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L4: Entry 2 of 6 File: USPT May 2, 2000

DOCUMENT-IDENTIFIER: US 6057125 A
TITLE: Clock gene and gene product

DEPU:
Vitatema, M. H., D. P. King, A.-M. Chang, J. M. Kornhauser, P. L. Lowrey, J. D. McDonald, W. F. Dove, L. P. Pinto, F. W. Turek, J. S. Takahashi. 1994. Mutagenesis and mapping of a mouse gene, Clock, essential for circadian behavior. Science 264:719-725

DEPU:
Vitatema, M. H., D. P. King, A.-M. Chang, J. M. Kornhauser, P. L. Lowrey, J. D. McDonald, W. F. Dove, L. P. Pinto, F. W. Turek, J. S. Takahashi. 1994. Mutagenesis and mapping of a mouse gene, Clock, essential for circadian behavior. Science 264:719-725

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DB Name	Query	Hit Count	Set Name
USPT,PGPB,JPAB,EPAB,DWPI	congenic and l1	0	L7
USPT,PGPB,JPAB,EPAB,DWPI	shedlovsky-a$.in.	4	L6
USPT,PGPB,JPAB,EPAB,DWPI	dove-w$.in.	7	L5
USPT,PGPB,JPAB,EPAB,DWPI	mutagenesis adj1 mapping	6	L4
USPT,PGPB,JPAB,EPAB,DWPI	l2 same mutagenesis	3	L3
USPT,PGPB,JPAB,EPAB,DWPI	congenic	254	L2
USPT,PGPB,JPAB,EPAB,DWPI	modifier adj1 (locus or loci)	9	L1

L5 ANSWER 4 OF 4 MEDLINE
AN 1998207250 MEDLINE
DN 98207250
TI A high-resolution genetic **map** of the nervous locus on mouse chromosome 8.
AU De Jager P L; Harvey D; Polydorides A D; Zuo J; Heintz N
CS Howard Hughes Medical Institute, Laboratory of Molecular Biology, Rockefeller University, New York, New York 10021, USA.
NC GM07739 (NIGMS)
SO GENOMICS, (1998 Mar 15) 48 (3) 346-53.
Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199808
EW 19980802
AB The nervous (nr) mutant mouse displays two gross recessive traits: both an exaggeration of juvenile hyperactivity and a pronounced ataxia become apparent during the third and fourth postnatal weeks. Using an intersubspecific intercross, we have established a high-resolution **map** of a segment of mouse chromosome 8 that places the nr locus in a genomic segment defined by D8Rck1 on the centromeric end and D8Mit3 on the telomeric end. This **map** position places the nr locus within the BALB/cGr **congenic** region of the C3HeB/ FeJ-nr strain, confirming the accuracy of our study. We used this **map** position to identify and evaluate three genes-ankyrin 1, cortexin, and farnesyltransferase-as candidates for the nr gene. These three genes were eliminated from consideration but allowed us to establish the conservation of synteny between the region containing the nr locus and a segment of the short arm of human chromosome 8 (8p21-p11.2). Finally, the incomplete penetrance of the nr phenotype led us to perform a screen for **modifier loci**, and we present evidence that such a nervous **modifier locus** may exist on mouse chromosome 5.

```
=> d his

     (FILE 'HOME' ENTERED AT 16:41:46 ON 02 APR 2001)

     FILE 'MEDLINE' ENTERED AT 16:41:53 ON 02 APR 2001
L1             0 S CONGENIC AND MUTAGENESIS MAPPING/AB,BI
L2             3 S MUTAGENESIS MAPPING/AB,BI
L3           108 S MODIFIER LOCUS OR MODIFIER LOCI/AB,BI
L4            10 S L3 AND CONGEN?/AB,BI
L5             4 S L4 AND MAP?/AB,BI
L6             0 S L3 AND L2

     FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS' ENTERED AT 16:46:21 ON
02
     APR 2001
L7             0 S L1
L8            42 S L2
L9           442 S L3
L10           62 S L4
L11          484 S L8 OR L9 OR L10
L12           39 S L11 AND BACKCROSS?/AB,BI
L13           13 DUP REM L12 (26 DUPLICATES REMOVED)
                 E DOVE WILLIAM F/AU
L14          133 S E2-E3
L15           12 S L14 AND L3
L16            7 DUP REM L15 (5 DUPLICATES REMOVED)
L17            0 S L14 AND L2
L18            0 S L14 AND L10
                 E SHEDLOVSKY ALEXANDRA/AU
L19           88 S E1-E4
L20           12 S L11 AND (L19 OR L14)
L21            7 DUP REM L20 (5 DUPLICATES REMOVED)
L22         5586 S ETHYLNITROSOUREA/AB,BI
L23         1788 S L22 AND MUTAGEN?/AB,BI
L24            1 S L23 AND L9
L25            7 S L23 AND BACKCROSS?/AB,BI
L26            4 DUP REM L25 (3 DUPLICATES REMOVED)
L27           39 S L9 AND BACKCROSS?/AB,BI
L28            2 S L27 AND MUTAGEN?/AB,BI
L29            2 DUP REM L28 (0 DUPLICATES REMOVED)
L30           13 DUP REM L27 (26 DUPLICATES REMOVED)
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=> d his


     (FILE 'HOME' ENTERED AT 16:41:46 ON 02 APR 2001)

     FILE 'MEDLINE' ENTERED AT 16:41:53 ON 02 APR 2001
L1             0 S CONGENIC AND MUTAGENESIS MAPPING/AB,BI
L2             3 S MUTAGENESIS MAPPING/AB,BI
L3           108 S MODIFIER LOCUS OR MODIFIER LOCI/AB,BI
L4            10 S L3 AND CONGEN?/AB,BI
L5             4 S L4 AND MAP?/AB,BI
L6             0 S L3 AND L2

     FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS' ENTERED AT 16:46:21 ON
02
     APR 2001
L7             0 S L1
L8            42 S L2
L9           442 S L3
L10           62 S L4
L11          484 S L8 OR L9 OR L10
L12           39 S L11 AND BACKCROSS?/AB,BI
L13           13 DUP REM L12 (26 DUPLICATES REMOVED)
                 E DOVE WILLIAM F/AU
L14          133 S E2-E3
L15           12 S L14 AND L3
L16            7 DUP REM L15 (5 DUPLICATES REMOVED)
L17            0 S L14 AND L2

=> s l14 and l10

L18            0 L14 AND L10

=> e shedlovsky alexandra/au

E1            61      SHEDLOVSKY A/AU
E2             3      SHEDLOVSKY A E/AU
E3            23 --> SHEDLOVSKY ALEXANDRA/AU
E4             1      SHEDLOVSKY ALEXANDRA J/AU
E5             8      SHEDLOVSKY J P/AU
E6             5      SHEDLOVSKY JULIAN P/AU
E7             3      SHEDLOVSKY LEO/AU
E8             5      SHEDLOVSKY THEODORE/AU
E9             3      SHEDLOW A M/AU
E10            1      SHEDLOW ALEXANDRA/AU
E11            7      SHEDLOW ALEXANDRA M/AU
E12            1      SHEDLOW ALEXANDRA MARY/AU

=> s e1-e4

L19           88 ("SHEDLOVSKY A"/AU OR "SHEDLOVSKY A E"/AU OR "SHEDLOVSKY
ALEXAND
                 RA"/AU OR "SHEDLOVSKY ALEXANDRA J"/AU)

=> s l11 and (l19 or l14)

L20           12 L11 AND (L19 OR L14)
```

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 ********** STN Columbus **********
**

FILE 'HOME' ENTERED AT 16:41:46 ON 02 APR 2001

=> file medline

COST IN U.S. DOLLARS                SINCE FILE     TOTAL
                                    ENTRY  SESSION
FULL ESTIMATED COST                   0.15     0.15

FILE 'MEDLINE' ENTERED AT 16:41:53 ON 02 APR 2001

 FILE LAST UPDATED: 22 MAR 2001 (20010322/UP). FILE
COVERS 1958 TO DATE.

 MEDLINE now contains new records from the former NLM
HEALTH STAR
 database. These records have an Entry Date and Update Date of
20010223.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2001 vocabulary. Enter HELP THESAURUS for details.

 The OLDMEDLINE file segment now contains data from 1958
through 1965.
 Enter HELP CONTENT for details.

 Left, right, and simultaneous left and right truncation are available in
the
 Basic Index. See HELP SFIELDS for details.

 THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY
AND ACCURATE
 SUBSTANCE IDENTIFICATION.

 MEDLINE has been updated with new records for the 2001
production year
 (20010322/UP). NLM is still in the process of preparing data.
Therefore,
 regular updates to the file are not in place. As soon as NLM makes
the
 regular updates available, we will process the update.

=> s congenic and mutagenesis mapping/ab,bi

      3481 CONGENIC
     57235 MUTAGENESIS/BI
    143268 MAPPING/BI
   5621341 AB/FA
         2 MUTAGENESIS MAPPING/AB
           ((MUTAGENESIS(W)MAPPING)/BI (L) AB/FA)
     57235 MUTAGENESIS/BI
    143268 MAPPING/BI
         3 MUTAGENESIS MAPPING/BI
           ((MUTAGENESIS(W)MAPPING)/BI)
L1       0 CONGENIC AND MUTAGENESIS MAPPING/AB,BI

=> s mutagenesis mapping/ab,bi

     57235 MUTAGENESIS/BI
    143268 MAPPING/BI
   5621341 AB/FA
         2 MUTAGENESIS MAPPING/AB
           ((MUTAGENESIS(W)MAPPING)/BI (L) AB/FA)
     57235 MUTAGENESIS/BI
    143268 MAPPING/BI
         3 MUTAGENESIS MAPPING/BI
           ((MUTAGENESIS(W)MAPPING)/BI)
L2       3 MUTAGENESIS MAPPING/AB,BI

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 3 ANSWERS -
CONTINUE? Y/(N):y


L2  ANSWER 1 OF 3  MEDLINE
AN  1998035455    MEDLINE
DN  98035455
TI  The crystal structure of vascular endothelial growth factor (VEGF)
refined
    to 1.93 A resolution: multiple copy flexibility and receptor binding.
AU  Muller Y A; Christinger H W; Keyt B A; de Vos A M
CS  Department of Protein Engineering, Genentech, Inc., South San
Francisco,
    CA 94080, USA.
SO  STRUCTURE, (1997 Oct 15) 5 (10) 1325-38.
    Journal code: B31. ISSN: 0969-2126.
CY  ENGLAND: United Kingdom
DT  Journal; Article; (JOURNAL ARTICLE)
LA  English
FS  Priority Journals
EM  199803
AB  BACKGROUND: Vascular endothelial growth factor (VEGF) is
an endothelial
    cell-specific angiogenic and vasculogenic mitogen. VEGF also
plays a role
    in pathogenic vascularization which is associated with a number of
    clinical disorders, including cancer and rheumatoid arthritis. The
    development of VEGF antagonists, which prevent the interaction of
VEGF
    with its receptor, may be important for the treatment of such
disorders.
    VEGF is a homodimeric member of the cystine knot growth factor
    superfamily, showing greatest similarity to platelet-derived growth
factor
    (PDGF). VEGF binds to two different tyrosine kinase receptors,
kinase
    domain receptor (KDR) and Fms-like tyrosine kinase 1 (Flt-1), and
a number
    of VEGF homologs are known with distinct patterns of specificity
for these
    same receptors. The structure of VEGF will help define the
location of the
    receptor-binding site, and shed light on the differences in specificity
    and cross-reactivity among the VEGF homologs. RESULTS: We
have determined
    the crystal structure of the receptor-binding domain of VEGF at
1.93 A
    resolution in a triclinic space group containing eight monomers in
the
    asymmetric unit. Superposition of the eight copies of VEGF shows
that the
    beta-sheet core regions of the monomers are very similar, with
slightly
    greater differences in most loop regions. For one loop, the different
    copies represent different snapshots of a concerted motion.
     ***Mutagenesis***    ***mapping***  shows that this loop is
part of the
    receptor-binding site of VEGF. CONCLUSIONS: A comparison of
the eight
    independent copies of VEGF in the asymmetric unit indicates the
    conformational space sampled by the protein in solution; the root
mean
    square differences observed are similar to those seen in ensembles
of the
    highest precision NMR structures. Mapping the receptor-binding
    determinants on a multiple sequence alignment of VEGF
homologs, suggests
    the differences in specificity towards KDR and Flt-1 may derive
from both
    sequence variation and changes in the flexibility of binding loops.
The
    structure can also be used to predict possible receptor-binding
    determinants for related cystine knot growth factors, such as PDGF.

L2  ANSWER 2 OF 3  MEDLINE
AN  83223569    MEDLINE
DN  83223569
TI  Localization of a Plasmodium surface antigen epitope by Tn5
     ***mutagenesis***    ***mapping***  of a recombinant cDNA
clone.
AU  Lupski J R; Ozaki L S; Ellis J; Godson G N
SO  SCIENCE, (1983 Jun 17) 220 (4603) 1285-8.
    Journal code: UJ7. ISSN: 0036-8075.
CY  United States
DT  Journal; Article; (JOURNAL ARTICLE)
LA  English
FS  Priority Journals; Cancer Journals
EM  198309
AB  A recombinant complementary DNA clone from Plasmodium
knowlesi makes a
    beta-lactamase fusion polypeptide in Escherichia coli that reacts
with a
    monoclonal antibody to a Plasmodium surface antigen. An epitope
of the
    surface antigen was localized by transposon Tn5
***mutagenesis***
```

mapping of the complementary DNA clone. The Tn5 mutation having
the farthest 5' insert into the complementary DNA portion of the chimeric
gene, giving the shortest truncated protein that maintained the ability to
bind monoclonal antibody, defined the location of the epitope.

L2 ANSWER 3 OF 3 MEDLINE
AN 81215331 MEDLINE
DN 81215331
TI Nitrosoguanidine sequential ***mutagenesis*** ***mapping*** of
Mycobacterium tuberculosis genes.
AU Woodley C L; Baldwin J N; Greenberg J
SO JOURNAL OF BACTERIOLOGY, (1981 Jul) 147 (1) 176-80.
Journal code: HH3. ISSN: 0021-9193.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198110
AB Nitrosoguanidine-induced mutations occur at higher frequencies at the
replication region than at other nonreplicating regions of the chromosome.
Cultures of Mycobacterium tuberculosis synchronized with phenylethanol
were used to determine the order of replication for 10 genes controlling
drug resistance. Use of M. tuberculosis provided a 10-h replication map
with good resolution because of the slow rate of deoxyribonucleic acid
replication. The direction of chromosome replication could not be
determined, but this study indicated no pause between rounds of
deoxyribonucleic acid replication in a rich medium.

=> s modifier locus or modifier loci/ab,bi

2973 MODIFIER
57107 LOCUS
67 MODIFIER LOCUS
(MODIFIER(W)LOCUS)
2973 MODIFIER/BI
29848 LOCI/BI
5621341 AB/FA
51 MODIFIER LOCI/AB
((MODIFIER(W)LOCI)/BI (L) AB/FA)
2973 MODIFIER/BI
29848 LOCI/BI
53 MODIFIER LOCI/BI
((MODIFIER(W)LOCI)/BI)
L3 108 MODIFIER LOCUS OR MODIFIER LOCI/AB,BI

=> s l3 and congen?/ab,bi

146823 CONGEN?/BI
5621341 AB/FA
62849 CONGEN?/AB
(CONGEN?/BI (L) AB/FA)
146823 CONGEN?/BI
L4 10 L3 AND CONGEN?/AB,BI

=> s l4 and map?/ab,bi

192862 MAP?/BI
5621341 AB/FA
97484 MAP?/AB
(MAP?/BI (L) AB/FA)
192862 MAP?/BI
L5 4 L4 AND MAP?/AB,BI

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y

L5 ANSWER 1 OF 4 MEDLINE
AN 2001122351 MEDLINE
DN 21015401
TI ROSA26 mice carry a modifier of Min-induced mammary and intestinal tumor
development.
AU Kohlhepp R L; Hegge L F; Nett J E; Moser A R
CS Department of Human Oncology, University of Wisconsin-Madison 53792, USA.
NC CA64843 (NCI)
SO MAMMALIAN GENOME, (2000 Dec) 11 (12) 1058-62.
Journal code: BES. ISSN: 0938-8990.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200102
AB B6.129S7-Gtrosa26 (B6.R26) mice carry a LacZ-neoR insertion on Chromosome
(Chr) 6, made by promoter trapping with 129 ES cells. Female C57BL/6J
ApcMin/+ (B6Min/+) mice are highly susceptible to intestinal tumors and to
the induction of mammary tumors after treatment with ethylnitrosourea
(ENU). However, B6.R26/+ Min/+ females develop fewer mammary and
intestinal tumors after ENU treatment than do B6 Min/+ mice. B6.R26/+ mice
from two independently derived ***congenic*** lines show this modifier
effect. Each of these ***congenic*** lines carries approximately 20 cM
of 129-derived DNA flanking the insertion, raising the possibility that
the resistance is due to a linked ***modifier*** ***locus***. To
further ***map*** the ***modifier*** ***locus***, we have
generated several lines of mice carrying different regions of the
congenic interval. We have found that resistance to mammary and
intestinal tumors in ENU-treated Min/+ mice ***maps*** to a minimum
4-cM interval that includes the ROSA26 LacZ-neoR insertion. Therefore, the
resistance to tumor development is due to either the ROSA26 insertion or a
very tightly linked ***modifier*** ***locus***.

L5 ANSWER 2 OF 4 MEDLINE
AN 2001101547 MEDLINE
DN 20545364
TI ***Mapping*** of melanoma ***modifier*** ***loci*** in RET
transgenic mice.
AU Dragani T A; Peissel B; Zanesi N; Aloisi A; Dai Y; Kato M; Suzuki H;
Nakashima I
CS Department of Experimental Oncology, Istituto Nazionale Tumori, Via G.
Venezian Milan, Italy.. dragani@istitutotumori.mi.it
SO JAPANESE JOURNAL OF CANCER RESEARCH, (2000 Nov) 91 (11) 1142-7.
Journal code: HBA. ISSN: 0910-5050.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200102
AB Transgenic mice carrying the RET oncogene under the control of the
metallothionein promoter exhibit severe pigmentation of the whole skin and
melanocytic tumors. The genetic background influences melanoma development
in RET mice; founder mice crossed with BALB/c mice show decreased
incidence and increased latency of melanocytic tumors, whereas progeny of
C57BL/6 mice show the opposite effect. Using partially ***congenic***
RET mice on a C57BL/6 genetic background (N3/RET mice), we studied genetic
linkage in (N3/RETxBALB/c)xN3/RET backcross mice. We ***mapped***
three melanoma ***modifier*** ***loci***, on chromosome 1 (Melm1
and Melm2) and chromosome 11 (Melm3), that are linked with early melanoma
incidence and latency. ***Mapping*** of Melm loci and of five
additional regions on chromosomes 6, 8, 9, 12, and 13 indicated

allelic
imbalance in N3/RET mice, with a significant excess of BALB/c alleles,
suggesting the presence of additional putative melanoma ***modifier***
loci on these chromosomes.

L5 ANSWER 3 OF 4 MEDLINE
AN 2001089278 MEDLINE
DN 20565764
TI Efficiency alleles of the Pctr1 ***modifier*** ***locus*** for
plasmacytoma susceptibility.
AU Zhang S L; DuBois W; Ramsay E S; Bliskovski V; Morse H C; Taddesse-Heath
L; Vass W C; DePinho R A; Mock B A
CS Laboratory of Genetics, Division of Basic Sciences, National Cancer
Institute, National Institutes of Health, Bethesda, Maryland 20892, USA.
SO MOLECULAR AND CELLULAR BIOLOGY, (2001 Jan) 21 (1) 310-8.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101
AB The susceptibility of BALB/c mice to pristane-induced plasmacytomas is a
complex genetic trait involving multiple loci, while DBA/2 and C57BL/6
strains are genetically resistant to the plasmacytomagenic effects of
pristane. In this model system for human B-cell neoplasia, one of the
BALB/c susceptibility and ***modifier*** ***loci*** , Pctr1, was
mapped to a 5.7-centimorgan (cM) chromosomal region that included
Cdkn2a, which encodes p16(INK4a) and p19(ARF), and the coding sequences
for the BALB/c p16(INK4a) and p19(ARF) alleles were found to be
polymorphic with respect to their resistant Pctr1 counterparts in DBA/2
and C57BL/6 mice (45). In the present study, alleles of Pctr1, Cdkn2a, and
D4Mit15 from a resistant strain (BALB/cDAG) carrying DBA/2 chromatin were
introgressively backcrossed to the susceptible BALB/c strain. The
resultant C.DAG-Pctr1 Cdkn2a D4Mit15 ***congenic*** was more resistant
to plasmacytomagenesis than BALB/c, thus narrowing Pctr1 to a 1.5-cM
interval. Concomitantly, resistant C57BL/6 mice, from which both gene
products of the Cdkn2a gene have been eliminated, developed
pristane-induced plasma cell tumors over a shorter latency period than the
traditionally susceptible BALB/cAn strain. Biological assays of the
p16(INK4a) and p19(ARF) alleles from BALB/c and DBA/2 indicated that the
BALB/c p16(INK4a) allele was less active than its DBA/2 counterpart in
inducing growth arrest of mouse plasmacytoma cell lines and preventing
ras-induced transformation of NIH 3T3 cells, while the two p19(ARF)
alleles displayed similar potencies in both assays. We propose that the
BALB/c susceptibility/ ***modifier*** ***locus*** , Pctr1, is an
"efficiency" allele of the p16(INK4a) gene.

L5 ANSWER 4 OF 4 MEDLINE
AN 1998207250 MEDLINE
DN 98207250
TI A high-resolution genetic ***map*** of the nervous locus on mouse
chromosome 8.
AU De Jager P L; Harvey D; Polydorides A D; Zuo J; Heintz N
CS Howard Hughes Medical Institute, Laboratory of Molecular Biology,
Rockefeller University, New York, New York 10021, USA.
NC GM07739 (NIGMS)
SO GENOMICS, (1998 Mar 15) 48 (3) 346-53.
Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199808
EW 19980802
AB The nervous (nr) mutant mouse displays two gross recessive traits: both an
exaggeration of juvenile hyperactivity and a pronounced ataxia become
apparent during the third and fourth postnatal weeks. Using an
intersubspecific intercross, we have established a high-resolution
map of a segment of mouse chromosome 8 that places the nr locus in
a genomic segment defined by D8Rck1 on the centromeric end and D8Mit3 on
the telomeric end. This ***map*** position places the nr locus within
the BALB/cGr ***congenic*** region of the C3HeB/ FeJ-nr strain,
confirming the accuracy of our study. We used this ***map*** position
to identify and evaluate three genes-ankyrin 1, cortexin, and
farnesyltransferase-as candidates for the nr gene. These three genes were
eliminated from consideration but allowed us to establish the conservation
of synteny between the region containing the nr locus and a segment of the
short arm of human chromosome 8 (8p21-p11.2). Finally, the incomplete
penetrance of the nr phenotype led us to perform a screen for
modifier ***loci*** , and we present evidence that such a
nervous ***modifier*** ***locus*** may exist on mouse chromosome
5.

=> s l3 and l2

L6 0 L3 AND L2

=> file medline embase biosis inpadoc caplus

=> s l1

'AB' IS NOT A VALID FIELD CODE
L7 0 L1

=> s l2

'AB' IS NOT A VALID FIELD CODE
L8 42 L2

=> s l3

'AB' IS NOT A VALID FIELD CODE
L9 442 L3

=> s l4

'AB' IS NOT A VALID FIELD CODE
L10 62 L4

=> s l8 or l9 or l10

L11 484 L8 OR L9 OR L10

=> s l11 and backcross?/ab,bi

'AB' IS NOT A VALID FIELD CODE
L12 39 L11 AND BACKCROSS?/AB,BI

=> dup rem l12

PROCESSING COMPLETED FOR L12
L13 13 DUP REM L12 (26 DUPLICATES REMOVED)

=> d l- bib ab

YOU HAVE REQUESTED DATA FROM 13 ANSWERS - CONTINUE? Y/(N):y

L13 ANSWER 1 OF 13 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 1
AN 2001:151886 BIOSIS
DN PREV200100151886
TI Epistatic interactions between skin tumor ***modifier*** ***loci***
in interspecific (spretus/musculus) ***backcross*** mice.
AU Nagase, Hiroki; Mao, Jian-Hua; de Koning, John P.; Minami, Tomoe; Balmain,
Allan (1)
CS (1) University of California-San Francisco Comprehensive Cancer Center,
2340 Sutter Street, San Francisco, CA, 94143 USA
SO Cancer Research, (February 15, 2001) Vol. 61, No. 4, pp. 1305-1308. print.
ISSN: 0008-5472.
DT Article
LA English
SL English
AB The development of cancer is influenced both by exposure to environmental
carcinogens and by the host genetic background. Epistatic interactions
between genes are important in determining phenotype in plant and animal
systems and are likely to be major contributors to cancer susceptibility
in humans. Several tumor ***modifier*** ***loci*** have been
identified from studies of mouse models of human cancer, and genetic
interactions between ***modifier*** ***loci*** have been detected
by genome scanning using recombinant ***congenic*** strains of mice
(R. Fijneman et al., Nat. Genet., 14: 465-467, 1996; T. van Wezel et al.,
Nat. Genet., 14: 468-470, 1996; W. N. Frankel et al., Nat. Genet., 14,
371-373, 1996). We demonstrate here that strong genetic interactions
between skin tumor ***modifier*** ***loci*** can be detected by
hierarchical whole genome scanning of a complete interspecific
backcross (outbred Mus spretus X Mus musculus (NIH/Ola)). A locus
on chromosome 7 (Skts1) showed a highly significant interaction with Skts5
on chromosome 12 ($P < 10-16$), whereas additional significant interactions
were detected between loci on chromosomes 4 and 5, and 16 and 15. Some of
these quantitative trait loci and their interactions, in particular the
Skts1-Skts5 interaction, were confirmed in two completely independent
backcrosses using inbred spretus strains (SEG/Pas and SPRET/Ei)
and NIH/Ola. These results, therefore, illustrate the general use of
interspecific crosses between Mus musculus and Mus spretus for the
detection of strong genetic interactions between tumor modifier genes.

L13 ANSWER 2 OF 13 MEDLINE DUPLICATE 2
AN 2001089278 MEDLINE
DN 20565764
TI Efficiency alleles of the Pctr1 ***modifier*** ***locus*** for
plasmacytoma susceptibility.
AU Zhang S L; DuBois W; Ramsay E S; Bliskovski V; Morse H C; Taddesse-Heath
L; Vass W C; DePinho R A; Mock B A
CS Laboratory of Genetics, Division of Basic Sciences, National Cancer
Institute, National Institutes of Health, Bethesda, Maryland 20892, USA.
SO MOLECULAR AND CELLULAR BIOLOGY, (2001 Jan) 21 (1) 310-8.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101
AB The susceptibility of BALB/c mice to pristane-induced plasmacytomas is a
complex genetic trait involving multiple loci, while DBA/2 and C57BL/6
strains are genetically resistant to the plasmacytomagenic effects of
pristane. In this model system for human B-cell neoplasia, one of the
BALB/c susceptibility and ***modifier*** ***loci*** , Pctr1, was
mapped to a 5.7-centimorgan (cM) chromosomal region that included Cdkn2a,
which encodes p16(INK4a) and p19(ARF), and the coding sequences for the
BALB/c p16(INK4a) and p19(ARF) alleles were found to be polymorphic with
respect to their resistant Pctr1 counterparts in DBA/2 and C57BL/6 mice
(45). In the present study, alleles of Pctr1, Cdkn2a, and D4Mit15 from a
resistant strain (BALB/cDAG) carrying DBA/2 chromatin were introgressively
backcrossed to the susceptible BALB/c strain. The resultant
C.DAG-Pctr1 Cdkn2a D4Mit15 ***congenic*** was more resistant to
plasmacytomagenesis than BALB/c, thus narrowing Pctr1 to a 1.5-cM
interval. Concomitantly, resistant C57BL/6 mice, from which both gene
products of the Cdkn2a gene have been eliminated, developed
pristane-induced plasma cell tumors over a shorter latency period than the
traditionally susceptible BALB/cAn strain. Biological assays of the
p16(INK4a) and p19(ARF) alleles from BALB/c and DBA/2 indicated that the
BALB/c p16(INK4a) allele was less active than its DBA/2 counterpart in
inducing growth arrest of mouse plasmacytoma cell lines and preventing
ras-induced transformation of NIH 3T3 cells, while the two p19(ARF)
alleles displayed similar potencies in both assays. We propose that the
BALB/c susceptibility/ ***modifier*** ***locus*** , Pctr1, is an
"efficiency" allele of the p16(INK4a) gene.

L13 ANSWER 3 OF 13 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease
locus and their use in screening for human homologs
IN Dove, William F.; Shedlovsky, Alexandra
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000004186	A1	20000127	WO 1999-US15661	19990712

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,
MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9949843	A1	20000207	AU 1999-49843	19990712

PRAI US 1998-114973 19980714
WO 1999-US15661 19990712
AB A method for breeding mutagenized mice that permits detection

of genetic
loci that can modify a known index phenotype involves crossing a mutagenized founder strain and a second strain of mice carrying an allele
at a locus that confers the index phenotype. In the test generation, clusters of individuals are obsd. to deviate from the typical phenotype.
The genetic material and mols. encoded thereby can be obtained using
available methods. Improved and compact methods called ICMM (index-directed, cluster-enhanced, ***Modifier*** ***locus*** and
Molecule identification method) are also disclosed. The method is exemplified by identification of the suppressor or enhancer alleles of
mouse Min allele of APC locus by phenotypic and genotypic studies of F1
generation (and their outcross and ***backcross*** offsprings) of
ethylnitrosourea mutagenized female BTBR and heterozygous B6-APCmin/+
male. The identification of these new genes in the mouse disease models
for human colon cancers are helpful to screen human homologs involved in
the related diseases.
RE.CNT 4
RE
(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Moml modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

L13 ANSWER 4 OF 13 MEDLINE DUPLICATE 3
AN 2001101547 MEDLINE
DN 20545364
TI Mapping of melanoma ***modifier*** ***loci*** in RET transgenic
mice.
AU Dragani T A; Peissel B; Zanesi N; Aloisi A; Dai Y; Kato M; Suzuki H;
Nakashima I
CS Department of Experimental Oncology, Istituto Nazionale Tumori, Via G.
Venezian Milan, Italy.. dragani@istitutotumori.mi.it
SO JAPANESE JOURNAL OF CANCER RESEARCH, (2000 Nov) 91 (11) 1142-7.
Journal code: HBA. ISSN: 0910-5050.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200102
AB Transgenic mice carrying the RET oncogene under the control of the
metallothionein promoter exhibit severe pigmentation of the whole skin and
melanocytic tumors. The genetic background influences melanoma development
in RET mice; founder mice crossed with BALB/c mice show decreased
incidence and increased latency of melanocytic tumors, whereas progeny of
C57BL/6 mice show the opposite effect. Using partially ***congenic***
RET mice on a C57BL/6 genetic background (N3/RET mice), we studied genetic
linkage in (N3/RETxBALB/c)xN3/RET ***backcross*** mice. We mapped
three melanoma ***modifier*** ***loci*** , on chromosome 1 (Melm1
and Melm2) and chromosome 11 (Melm3), that are linked with early melanoma
incidence and latency. Mapping of Melm loci and of five additional regions
on chromosomes 6, 8, 9, 12, and 13 indicated allelic imbalance in N3/RET
mice, with a significant excess of BALB/c alleles, suggesting the presence
of additional putative melanoma ***modifier*** ***loci*** on these
chromosomes.

L13 ANSWER 5 OF 13 CAPLUS COPYRIGHT 2001 ACS
AN 2000:80654 CAPLUS
DN 132:235822
TI Genetic regulation of anti-erythrocyte autoantibodies and splenomegaly in
autoimmune hemolytic anemia-prone New Zealand Black mice
AU Ochiai, Kimiko; Ozaki, Shoichi; Tanino, Akihiro; Watanabe, Shinji; Ueno,
Tomoo; Mitsui, Kenichi; Toei, Junichi; Inada, Yuji; Hirose, Sachiko;
Shirai, Toshikazu; Nishimura, Hiroyuki
CS Toin Human Science and Technology Center, Department of Biomedical
Engineering, Toin University of Yokohama, Yokohama, 225-8502, Japan
SO Int. Immunol. (2000), 12(1), 1-8
CODEN: INIMEN; ISSN: 0953-8178
PB Oxford University Press
DT Journal
LA English
AB New Zealand Black (NZB) mice spontaneously produce anti-erythrocyte
autoantibodies (AEA) in assocn. with splenomegaly, thus serving as a model
for autoimmune hemolytic anemia. Although these autoimmune traits are
inherited as a dominant fashion, expression in F1 hybrids of NZB and most
non-New Zealand strains is suppressed due to the contribution of wild-type
modifying genes present in the latter strains. Using chromosomal
microsatellite markers in the (C57BL/6 .times. NZB)F1 .times. NZB
backcross progeny, the authors mapped C57BL/6 modifying loci for
AEA prodn. and splenomegaly. Generation of AEA was down-regulated by a
combined effect of two major independently segregating dominant alleles,
one linked to D7MIT30 on chromosome 7 and the other linked to D10MIT42 on
chromosome 10. Splenomegaly was modified mainly by a single C57BL/6
allele linked to D4MIT58 on chromosome 4. Thus, the autoimmune hemolytic
anemia in the NZB strain is under multigenic control and a combined action
of not only susceptibility but also modifying alleles with suppressive
activities affects the outcome of disease features in the progeny. There
are potentially important candidate genes which may be linked to the
regulation of AEA and splenomegaly.
RE.CNT 31
RE
(4) Dietrich, W; Genetics 1992, V131, P423 CAPLUS
(5) Drake, C; Proc Natl Acad Sci USA 1994, V91, P4062 CAPLUS
(7) Egle, A; Eur J Immunol 1996, V26, P3119 CAPLUS
(9) Hirose, S; Int Immunol 1994, V6, P1857 CAPLUS
(12) Jiang, Y; J Immunol 1997, V158, P992 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 6 OF 13 MEDLINE DUPLICATE 4
AN 2000079602 MEDLINE
DN 20079602
TI A subset of skin tumor ***modifier*** ***loci*** determines
survival time of tumor-bearing mice.
AU Nagase H; Mao J H; Balmain A
CS University of California San Francisco Cancer Center, Cancer Research
Institute, University of California, 2340 Sutter Street, San Francisco, CA
94105, USA.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1999 Dec 21) 96 (26) 15032-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 200003
EW 20000305
AB Studies of mouse models of human cancer have established the existence of
multiple tumor modifiers that influence parameters of cancer susceptibility such as tumor multiplicity, tumor size, or the probability
of malignant progression. We have carried out an analysis of skin tumor
susceptibility in interspecific Mus musculus/Mus spretus hybrid mice and
have identified another seven loci showing either significant (six loci)
or suggestive (one locus) linkage to tumor susceptibility or resistance. A
specific search was carried out for skin tumor ***modifier*** ***loci*** associated with time of survival after development of a
malignant tumor. A combination of resistance alleles at three markers
[D6Mit15 (Skts12), D7Mit12 (Skts2), and D17Mit7 (Skts10)], all of which
are close to or the same as loci associated with carcinoma incidence and/or papilloma multiplicity, is significantly associated with increased
survival of mice with carcinomas, whereas the reverse combination of
susceptibility alleles is significantly linked to early mortality caused by rapid carcinoma growth (chi(2) = 25.22; P = 5.1 x 10(-8)). These data
indicate that host genetic factors may be used to predict carcinoma growth
rate and/or survival of individual ***backcross*** mice exposed to the
same carcinogenic stimulus and suggest that mouse models may provide an
approach to the identification of genetic modifiers of cancer survival in
humans.

L13 ANSWER 7 OF 13 MEDLINE DUPLICATE 5
AN 1998054360 MEDLINE
DN 98054360
TI Epilepsy in mice deficient in the 65-kDa isoform of glutamic acid decarboxylase.
AU Kash S F; Johnson R S; Tecott L H; Noebels J L; Mayfield R D; Hanahan D;
Baekkeskov S
CS Department of Medicine, School of Medicine, University of California at
San Francisco, San Francisco, CA 94143, USA.
NC DK41822 (NIDDK)
NS29709/11535 (NINDS)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1997 Dec 9) 94 (25) 14060-5.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199803
EW 19980303
AB gamma-Aminobutyric acid (GABA), the major inhibitory neurotransmitter in
the mammalian brain, is synthesized by two glutamate decarboxylase
isoforms, GAD65 and GAD67. The separate role of the two isoforms is
unknown, but differences in saturation with cofactor and subcellular localization suggest that GAD65 may provide reserve pools of GABA for
regulation of inhibitory neurotransmission. We have disrupted the gene
encoding GAD65 and ***backcrossed*** the mutation into the C57BL/6
strain of mice. In contrast to GAD67-/- animals, which are born with
developmental abnormalities and die shortly after birth, GAD65-/- mice
appear normal at birth. Basal GABA levels and holo-GAD activity are
normal, but the pyridoxal 5' phosphate-inducible apo-enzyme reservoir is
significantly decreased. GAD65-/- mice develop spontaneous seizures that
result in increased mortality. Seizures can be precipitated by fear or mild stress. Seizure susceptibility is dramatically increased in GAD65-/-
mice ***backcrossed*** into a second genetic background, the nonobese
diabetic (NOD/LtJ) strain of mice enabling electroencephalogram analysis
of the seizures. The generally higher basal brain GABA levels in this
backcross are significantly decreased by the GAD65-/- mutation,
suggesting that the relative contribution of GABA synthesized by GAD65 to
total brain GABA levels is genetically determined. Seizure-associated
c-fos-like immunoreactivity reveals the involvement of limbic regions of
the brain. These data suggest that GABA synthesized by GAD65 is important
in the dynamic regulation of neural network excitability, implicate at
least one ***modifier*** ***locus*** in the NOD/LtJ strain, and
present GAD65-/- animals as a model of epilepsy involving GABA-ergic
pathways.

L13 ANSWER 8 OF 13 MEDLINE DUPLICATE 6
AN 96172827 MEDLINE
DN 96172827
TI Modulation of disease severity in cystic fibrosis transmembrane conductance regulator deficient mice by a secondary genetic factor [published erratum appears in Nat Genet 1996 May;13(1):129].
AU Rozmahel R; Wilschanski M; Matin A; Plyte S; Oliver M; Auerbach W; Moore
A; Forstner J; Durie P; Nadeau J; Bear C; Tsui L C
CS Department of Molecular Genetics, The University of Toronto, Ontario,
Canada.
SO NATURE GENETICS, (1996 Mar) 12 (3) 280-7.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB Mice that have been made deficient for the cystic fibrosis transmembrane
conductance regulator (Cftr) usually die of intestinal obstruction. We
have created Cftr-deficient mice and demonstrate prolonged survival among
backcross and intercross progeny with different inbred strains,
suggesting that modulation of disease severity is genetically determined.
A genome scan showed that the major ***modifier*** ***locus***
maps near the centromere of mouse chromosome 7. Electrophysiological
studies on mice with prolonged survival show that the partial rectification of Cl- and Na+ ion transport abnormalities can be explained
in part by up-regulation of a calcium-activated Cl- conductance. Identification of modifier genes in our Cftr(m1HSC)/Cftr(m1HSC) mice
should provide important insight into the heterogeneous disease presentation observed among CF patients.

L13 ANSWER 9 OF 13 MEDLINE DUPLICATE 7
AN 96121384 MEDLINE
DN 96121384
TI A curly-tail ***modifier*** ***locus*** , mct1, on mouse chromosome
17.
AU Letts V A; Schork N J; Copp A J; Bernfield M; Frankel W N
CS Jackson Laboratory, Bar Harbor, Maine 04609, USA.
NC HD28882 (NICHD)
SO GENOMICS, (1995 Oct 10) 29 (3) 719-24.

Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB The major gene for neural tube defects, ct, in the curly-tail (CT) mouse
strain was mapped previously to mouse chromosome 4 by combining linkage
data from several ***backcrosses*** . The penetrance of the neural tube
trait, already incomplete in the CT strain, was further reduced in several
of these ***backcrosses*** , suggesting the existence of recessive
modifiers or strain-specific susceptibility alleles. Here we describe the
mapping of a curly-tail ***modifier*** ***locus*** , mct1, to
chromosome 17 in moderate and low penetrance crosses of CT with BALB/cByJ
and Mus spretus. No effect of mct1 was seen in a higher penetrance cross
with the BXD-8/Ty strain, confirming that ct is the major gene in the
model. Homozygosity at both ct and mct1 loci was sufficient to account for
all of the affected individuals in the BALB/cByJ cross and most of the
affected individuals in the M. spretus cross and was the preferred model
overall. No evidence was found for epistatic interaction between ct and
mct1.

L13 ANSWER 10 OF 13 MEDLINE DUPLICATE 8
AN 96106991 MEDLINE
DN 96106991
TI Steroid sulfatase and the Y chromosome hypertensive locus of the
spontaneously hypertensive rat.
AU Johnson M L; Ely D L; Turner M E
CS Midwest Hypertension Research Center, Omaha, Nebraska, USA.
SO STEROIDS, (1995 Oct) 60 (10) 681-5.
Journal code: V10. ISSN: 0039-128X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199604
AB The spontaneously hypertensive rat (SHR) has a Y chromosome locus that
increases blood pressure. This locus requires an androgen receptor and
testosterone for maximum expression. Steroid sulfatase (STS) catalyzes the
conversion of steroid sulfates to their active nonconjugated form. In some
mammals the steroid sulfatase locus (Sts) is on the Y chromosome, although
the rat Sts is on the X chromosome. We measured STS activity levels in SHR
and normotensive Wistar Kyoto (WKY) males. SHR had significantly higher
STS activity in testes, adrenal gland, liver, and hypothalamus. The Km
values for STS in the two strains were not significantly different; thus,
activity differences were likely due to differences in enzyme amounts. STS
activity was measured in the ***backcross*** strains SHR/y and SHR/a
to test and/or confirm a Y chromosome influence on STS. STS activity
levels in these strains were intermediate between those of SHR and WKY.
Because the blood pressures of SHR/y and SHR/a were also intermediate
between SHR and WKY, the STS activity could be a secondary response to the
hypertension. An alternative hypotheses is that a regulatory locus in
addition to the structural locus is responsible for STS activity levels,
and this regulatory locus is on the rat Y chromosome. Further study is
needed to discriminate between these possibilities, and until the second
hypothesis can be eliminated, the Sts locus or its ***modifier***
loci remain a potential component of the Y chromosome hypertensive
locus.

L13 ANSWER 11 OF 13 MEDLINE DUPLICATE 9
AN 94061981 MEDLINE
DN 94061981
TI Genetic identification of Mom-1, a major ***modifier*** ***locus***
affecting Min-induced intestinal neoplasia in the mouse.
AU Dietrich W F; Lander E S; Smith J S; Moser A R; Gould K A; Luongo C;
Borenstein N; Dove W
CS Whitehead Institute for Biomedical Research, Massachusetts Institute of
Technology, Cambridge 02142.
NC HG00098 (NHGRI)
HG00126 (NHGRI)
CA07075 (NCI)
+
SO CELL, (1993 Nov 19) 75 (4) 631-9.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199403
AB Mutations in the human APC gene caused various familial colon cancer
syndromes. The Multiple intestinal neoplasia (Min) mouse provides an
excellent model for familial colon cancer: it carries a mutant mouse Apc
gene and develops many intestinal adenomas. Here, we analyze how this
tumor phenotype is dramatically modified by genetic background. We report
the genetic mapping of a locus that strongly modifies tumor number in
Min/+ animals. This gene, Mom-1 (Modifier of Min-1), maps to distal
chromosome 4 and controls about 50% of genetic variation in tumor number
in two intraspecific ***backcrosses*** . The mapping is supported by a
LOD score exceeding 14. Interestingly, Mom-1 lies in a region of synteny
conservation with human chromosome 1p35-36, a region of frequent somatic
loss of heterozygosity in a variety of human tumors, including colon
tumors. These results provide evidence of a major modifier affecting
expression of an inherited cancer syndrome.

L13 ANSWER 12 OF 13 MEDLINE DUPLICATE 10
AN 92176249 MEDLINE
DN 92176249
TI The Min (multiple intestinal neoplasia) mutation: its effect on gut
epithelial cell differentiation and interaction with a modifier system.
AU Moser A R; Dove W F; Roth K A; Gordon J I
CS McArdle Laboratory, University of Wisconsin, Madison 53706..
NC CA07075 (NCI)
CA50585 (NCI)
CA23076 (NCI)
+
SO JOURNAL OF CELL BIOLOGY, (1992 Mar) 116 (6) 1517-26.
Journal code: HMV. ISSN: 0021-9525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199206
AB Min is a fully penetrant dominant mutation that leads to the development
of multiple intestinal adenomas throughout the duodenal-to-colonic axis.
Min/+ C57BL6/J mice have an average life-span of 120 d.
Multi-label
immunocytochemical studies of these lesions demonstrate patches

of
differentiated enterocytes, and scattered enteroendocrine, goblet and
Paneth cells. Expression of endogenous marker genes within these
differentiated cells can be directly correlated with the position occupied
by the adenoma along the duodenal-to-colonic axis and mirrors the regional
differentiation of the normal gut epithelium. The presence of multiple
lineages in adenomas together with their retention of spatial information
suggests that tumorigenesis in Min/+ mice may be initiated in a
multipotent stem cell normally located at the base of intestinal crypts.
To study the time-dependent properties of these tumors, genetic conditions
were sought in which Min/+ animals could survive for up to 300 d. Min is
fully penetrant in hybrids with either AKR/J or MA/MyJ. However, the
hybrids demonstrate a reduction in the number of intestinal adenomas.
Preliminary ***backcross*** analysis is consistent with a single major
modifier ***locus*** unlinked to Min in both the AKR/J and
MA/MyJ strains. The increased lifespan of the hybrid animals is also
associated with the development of invasive tumors. New tumors do not
arise continuously over the lifespan of these animals; instead all
adenomas appear to be established by 100 d of age or sooner. These studies
indicate that the Min/+ mouse is a powerful model system for analyzing the
mechanisms that establish and maintain a balance between proliferation and
differentiation in the continuously renewing gut epithelium and for an
assessment of the multi-step hypothesis of intestinal neoplasia.

L13 ANSWER 13 OF 13 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1990:43589 BIOSIS
DN BA89:20953
TI EVALUATION OF F-2 X F-2 AND BC-1 X BC-1 MAIZE INTERPOPULATION CROSSES.
AU BERNARDO R; JOHNSON G R; DUDLEY J W; MEGHJI M R
CS DEP. AGRON., UNIV. ILL., 1102 S. GOODWIN AVE., URBANA, ILL. 61801.
SO CROP SCI. (1989) 29 (6), 1377-1381.
CODEN: CRPSAY. ISSN: 0011-183X.
FS BA; OLD
LA English
AB Further improvement in the performance of elite maize (Zea mays L.)
hybrids is an important objective of maize breeding programs.
Introgression of broadbase germplasm to improve the elite single cross B73
.times. Mo17H was considered. Estimates of genetic parameters in a [B73 73
.times. B Composite]F2 .times. [Mo17H .times. A Composite]F2 Design 2
population and a [B73(B73 .times. B Composite]BC1 .times. [Mo17H(Mo17H
.times. A Composite)]BC1 Design 2 population were obtained. Proportion of
broadbase germplasm had a linear effect on means with the order of
performance (most favorable to least favorable) for all traits being B73
.times. Mo17H, the BC1 interpopulation cross, the F2 interpopulation
cross, and A Composite .times. B Composite. Estimates of half-sib
covariances (CovHS) and specific combining ability variance (VarSCA) for
grain moisture and plant and ear heights were greater in the F2 than in
the BC1 interpopulation cross as expected for a one-locus, two-allele
genetic model. Contrary to expectations, estimates for grain yield of
CovHS in the population related to B73 and of VarSCA were two and four
times greater, respectively, in the BC1 than in the F2. The large
estimates of CovHS and VarSCA for grain yield in the BC, interpopulation
cross were consistent with expectations for a model in which B73 and Mo17H
are homozygous for an allele at a ***modifier*** ***locus***
which causes complete dominance at a quantitative trait locus. Frequency
of the modifier allele in the two composites would be near zero under this
model. The VarSCA results suggested the use of ***backcross***
populations for selection procedures that exploit specific combining
ability efects. Together with higher frequencies of BC1 .times. BC1
testcrosses superior to B73 .times. Mo17H, they indicated a higher
probability for immediate derivation of superior single crosses from the
BC1.

=> e dove william f/au

E1 1 DOVE WAYNE KEITH/AU
E2 7 DOVE WILLIAM/AU
E3 126 --> DOVE WILLIAM F/AU
E4 1 DOVE WILLIAM G/AU
E5 2 DOVE WILLIAM T/AU
E6 1 DOVE WILLIAM THOMASON/AU
E7 4 DOVE WINIFRED/AU
E8 1 DOVE Y/AU
E9 2 DOVE YVONNE/AU
E10 6 DOVECAR FRANK/AU
E11 1 DOVECAR GERT ING/AU
E12 1 DOVECAR STANKO/AU

=> s e2-e3

L14 133 ("DOVE WILLIAM"/AU OR "DOVE WILLIAM F"/AU)

=> s l14 and l3

'AB' IS NOT A VALID FIELD CODE
L15 12 L14 AND L3

=> dup rem l15

PROCESSING COMPLETED FOR L15
L16 7 DUP REM L15 (5 DUPLICATES REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 7 ANSWERS - CONTINUE? Y/(N):y

L16 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease
locus and their use in screening for human homologs
IN ***Dove, William F.*** ; Shedlovsky, Alexandra
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 2000004186 A1 20000127 WO 1999-US15661 19990712
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,
MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,

ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9949843 A1 20000207 AU 1999-49843 19990712
PRAI US 1998-114973 19980714
WO 1999-US15661 19990712
AB A method for breeding mutagenized mice that permits detection of genetic
loci that can modify a known index phenotype involves crossing a mutagenized founder strain and a second strain of mice carrying an allele
at a locus that confers the index phenotype. In the test generation, clusters of individuals are obsd. to deviate from the typical phenotype.
The genetic material and mols. encoded thereby can be obtained using
available methods. Improved and compact methods called ICMM (index-directed, cluster-enhanced, ***Modifier*** ***locus*** and
Molecule identification method) are also disclosed. The method is exemplified by identification of the suppressor or enhancer alleles of
mouse Min allele of APC locus by phenotypic and genotypic studies of F1
generation (and their outcross and backcross offsprings) of ethylnitrosourea mutagenized female BTBR and heterozygous B6-APCmin/+
male. The identification of these new genes in the mouse disease models
for human colon cancers are helpful to screen human homologs involved in
the related diseases.
RE.CNT 4
RE
(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Mom1 modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

L16 ANSWER 2 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
DUPLICATE 1
AN 2000:343967 BIOSIS
DN PREV200000343967
TI The Mom1AKR intestinal tumor resistance region consists of Pla2g2a and a
locus distal to D4Mit64.
AU Cormier, Robert T.; Bilger, Andrea; Lillich, Amy J.; Halberg, Richard B.;
Hong, Karen H.; Gould, Karen A.; Borenstein, Natalie; Lander, Eric S.;
Dove, William F. (1)
CS (1) McArdle Laboratory for Cancer Research, University of Wisconsin,
Madison, WI, 53706 USA
SO Oncogene, (29 June, 2000) Vol. 19, No. 28, pp. 3182-3192. print.
ISSN: 0950-9232.
DT Article
LA English
SL English
AB The Mom1 (Modifier of Min-1) region of distal chromosome 4 was identified
during a screen for polymorphic modifiers of intestinal tumorigenesis in
ApcMin/+ mice. Here, we demonstrate that the Mom1AKR allele consists of
two genetic components. These include the secretory phospholipase Pla2g2a,
whose candidacy as a Mom1 resistance modifier has now been tested with
several transgenic lines. A second region, distal to Pla2g2a, has also
been identified using fine structure recombinants. Pla2g2aAKR transgenic
mice demonstrate a modest resistance to tumorigenesis in the small intestine and a very robust resistance in the large intestine. Moreover,
the tumor resistance in the colon of Pla2g2aAKR animals is
dosage-dependent, a finding that is consistent with our observation that
Pla2g2a is expressed in goblet cells. By contrast, mice carrying the distal Mom1 modifier demonstrate a modest tumor resistance that is
confined to the small intestine. Thus, the phenotypes of these two ***modifier*** ***loci*** are complementary, both in their quantitative and regional effects. The additive effects and tight linkage
of these modifiers may have been necessary for the initial identification
of the Mom1 region.

L16 ANSWER 3 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:394514 BIOSIS
DN PREV199800394514
TI The intestinal epithelium and its neoplasms: Genetic, cellular and tissue
interactions.
AU ***Dove, William F.*** ; Cormier, Robert T.; Gould, Karen A.; Halberg, Richard B.; Merritt, Anita J.; Newton, Michael A.; Shoemaker, Alexander R.
CS McArdle Lab. Cancer Res., Univ. Wisconsin, Madison, WI 53706 USA
SO Philosophical Transactions of the Royal Society of London B Biological
Sciences, (June 29, 1998) Vol. 353, No. 1370, pp. 915-923.
ISSN: 0962-8436.
DT General Review
LA English
AB The Min (multiple intestinal neoplasia) strain of the laboratory mouse and
its derivatives permit the fundamental study of factors that regulate the
transition between normal and neoplastic growth. A gene of central importance in mediating these alternative patterns of growth is Apc, the
mouse homologue of the human adenomatous polyposis coli (APC) gene. When
adenomas form in the Min mouse, both copies of the Apc gene must be
inactivated. One copy is mutated by the nonsense Apc allele carried in
heterozygous form in this strain. The other copy can be silenced by any of
several mechanisms. These range from loss of the homologue bearing the
wild-type Apc allele; to interstitial deletions surrounding the wild-type
allele; to intragenic mutation, including nonsense alleles; and finally,
to a reduction in expression of the locus, perhaps owing to mutation in a
regulatory locus. Each of these proposed mechanisms may constitute a
two-hit genetic process as initially posited by Knudson; however, apparently the two hits could involve either a single locus or two loci.
The kinetic order for the transition to adenoma may be still higher than
two, if polyclonal adenomas require stronger interactions than passive
fusion. The severity of the intestinal neoplastic phenotype of the Min
mouse is strongly dependent upon loci other than Apc. One of these, Mom1,
has now been rigorously identified at the molecular level as encoding an
active resistance conferred by a secretory phospholipase. Mom1 acts
locally within a crypt lineage, not systemically. Within the crypt lineage, however, its action seems to be non-autonomous: when tumours
arise in Mom1 heterozygotes, the active resistance allele is maintained in
the tumour (MOH or maintenance of heterozygosity). Indeed, the secretory
phospholipase is synthesized by post-mitotic Paneth cells, not by the
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autonomy of modifier gene action in chimeric mice deserves detailed
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chimeric and to the clonal structure of the tissue in question. Beyond
Mom1, other loci can strongly modify the severity of the Min

phenotype. An
emergent challenge is to find ways to identify the full set of genes that
interact with the intestinal cancer predisposition of the Min mouse
strain. With such a set, one can then work, using contemporary mouse
genetics, to identify the molecular, cellular and organismal strategies
that integrate their functions. Finally, with appropriately phenotyped
human families, one can investigate by a candidate approach which
modifying factors influence the epidemiology of human colon cancer. Even
if a candidate modifier does not explain any of the genetic epidemiology
of colon cancer in human populations, modifier activities discovered by
mouse genetics provide candidates for chemopreventive and/or therapeutic
modalities in the human.

L16 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 2
AN 1997:298155 BIOSIS
DN PREV199799597358
TI Localized gene action controlling intestinal neoplasia in mice.
AU Gould, Karen A.; ***Dove, William F. (1)***
CS (1) McArdle Lab. Cancer Res., 1400 University Ave., Madison, WI 53706 USA
SO Proceedings of the National Academy of Sciences of the United States of
America, (1997) Vol. 94, No. 11, pp. 5848-5853.
ISSN: 0027-8424.
DT Article
LA English
AB Mice heterozygous for the Apc-Min (Min) mutation develop adenomas
throughout the intestinal tract. Apc is believed to be involved in cell
migration, adhesion, and polarity. Adenoma multiplicity and growth rate
are modulated by an unlinked ***modifier*** ***locus*** , Mom1. The
secretory phospholipase Pla2g2a is a candidate for Mom1. Here, we
investigate the range of action of Apc and Mom1. Analysis of chimeric Min
mice indicates that the actions of both Apc and Mom1 are localized within
the cell lineage that gives rise to intestinal tumors.

L16 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 3
AN 1997:438664 BIOSIS
DN PREV199799737867
TI Secretory phospholipase Pla2g2a confers resistance to intestinal tumorigenesis.
AU Cormier, Robert T.; Hong, Karen H.; Halberg, Richard B.; Hawkins, Trevor
L.; Richardson, Paul; Mulherkar, Rita; ***Dove, William F. (1)*** ;
Lander, Eric S.
CS (1) McArdle Lab. Cancer Research, Univ. Wisconsin, Madison, WI 53706 USA
SO Nature Genetics, (1997) Vol. 17, No. 1, pp. 88-91.
ISSN: 1061-4036.
DT Article
LA English
AB Individuals inheriting the same mutation predisposing to cancer may show
very different outcomes, ranging from early aggressive cancer to
disease-free survival. Experimental mouse models can provide a powerful
tool to identify factors in the environment and genetic background that
account for such modifications. The Min mouse strain, in which the Apc-Min
mutation disrupts the mouse homologue of the human familial polyposis
gene, develops intestinal neoplasms whose multiplicity is strongly
affected by genetic background. We previously mapped a strong
modifier ***locus*** , Mom1 (modifier of Min-1), to a 4-cM
region on mouse chromosome 4 containing a candidate gene Pla2g2a encoding
a secretory phospholipase. Here, we report that a cosmid transgene
overexpressing Pla2g2a caused a reduction in tumour multiplicity and size,
comparable to that conferred by a single copy of the resistance allele of
Mom1. These results offer strong evidence that this secretory
phospholipase can provide active tumour resistance. The association of
Pla2g2a with Mom1 thus withstands a strong functional test and is likely
to represent the successful identification of a polymorphic quantitative
trait locus in mammals.

L16 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 4
AN 1996:527044 BIOSIS
DN PREV199699249400
TI Action of Min and Mom1 on neoplasia in ectopic intestinal grafts.
AU Gould, Karen A.; ***Dove, William F. (1)***
CS (1) McArdle Lab. Cancer Research, 1400 University Ave., Madison, WI 53706
USA
SO Cell Growth & Differentiation, (1996) Vol. 7, No. 10, pp. 1361-1368.
ISSN: 1044-9523.
DT Article
LA English
AB Mice heterozygous for Min, a mutant allele of Apc, develop adenomas
throughout the intestinal tract. Tumor multiplicity in Min mice is
influenced by genetic ***modifier*** ***loci*** . Previously, we
mapped one of these ***modifier*** ***loci*** , Mom1, to distal
mouse chromosome 4. Mom1 is a semidominant modifier of both tumor size and
multiplicity in Min mice. Recent evidence suggests that Mom1 may encode a
secretory phospholipase, Pla2g2a. Pla2g2a is expressed in a variety of
cell types and seems to be involved in inflammatory responses and
bacterial defense mechanisms. Here, we determine whether Min and Mom1 act
in a tissue-autonomous fashion using ectopic intestinal isografts. Within
the small intestinal grafts, both Min and Mom1 act in a tissue-autonomous
manner. There is no evidence that either Min or Mom1 has a systemic effect
on tumor development. However, within the colonic grafts, the Min
phenotype does not appear to be autonomous; the development of colonic
tumors in Min mice seems dependent on factors beyond the Min genotype of
the colonic epithelium. Microenvironmental factors, such as digestive
secretions, dietary components, or intestinal flora, may be critical
factors contributing to the development of Min-induced colonic tumors.
However, these factors are not required for the action of Min or Mom1
within the small intestine.

L16 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 5
AN 1994:64047 BIOSIS
DN PREV199497077047
TI Genetic identification of Mom-1, a major ***modifier*** ***locus***
affecting Min-induced intestinal neoplasia in the mouse.
AU Dietrich, William F. (1); Lander, Eric S. (1); Smith, Jennifer S. (1);
Moser, Amy R.; Gould, Karen A.; Luongo, Cindy; Borenstein, Natalie;
Dove, William
CS (1) Whitehead Inst. Biomed Res., Dep. Biol., Mass. Inst. Technol.,
Cambridge, MA 02142 USA
SO Cell, (1993) Vol. 75, No. 4, pp. 631-639.
ISSN: 0092-8674.
DT Article
LA English
AB Mutations In the human A PC gene cause various familial colon cancer
syndromes. The Multiple intestinal neoplasia (Min) mouse provides an

excellent model for familial colon cancer: it carries a mutant mouse Apc
gene and develops many intestinal adenomas. Here, we analyze how this
tumor phenotype is dramatically modified by genetic background, We report
the genetic mapping of a locus that strongly modifies tumor number in
Min1+ animals. This gene, Mom-1 (Modifier of Min-1), maps to distal
chromosome 4 and controls about 50% of genetic variation In tumor number
in two by a LOD score exceeding 14. Interestingly, Mom-1 intraspecific
backcrosses. The mapping is supported by a LOD score exceeding 14.
Interesting, Mom-1 lies in a region of synteny conservation with human
chromsome 1p35-36, a region of frequent somatic loss of heterozygosity in
a variety of human tumors, including colon tumors. These results provide
evidence of a major modifier affecting expression of an inherited cancer
syndrome.

=> s l14 and l2

'AB' IS NOT A VALID FIELD CODE
L17 0 L14 AND L2

=> s l14 and l10

L18 0 L14 AND L10

=> e shedlovsky alexandra/au

E1	61	SHEDLOVSKY A/AU
E2	3	SHEDLOVSKY A E/AU
E3	23	--> SHEDLOVSKY ALEXANDRA/AU
E4	1	SHEDLOVSKY ALEXANDRA J/AU
E5	8	SHEDLOVSKY J P/AU
E6	5	SHEDLOVSKY JULIAN P/AU
E7	3	SHEDLOVSKY LEO/AU
E8	5	SHEDLOVSKY THEODORE/AU
E9	3	SHEDLOW A M/AU
E10	1	SHEDLOW ALEXANDRA/AU
E11	7	SHEDLOW ALEXANDRA M/AU
E12	1	SHEDLOW ALEXANDRA MARY/AU

=> s e1-e4

L19 88 ("SHEDLOVSKY A"/AU OR "SHEDLOVSKY A E"/AU OR "SHEDLOVSKY ALEXANDRA"/AU OR "SHEDLOVSKY ALEXANDRA J"/AU)

=> s l11 and (l19 or l14)

L20 12 L11 AND (L19 OR L14)

=> dup rem l20

PROCESSING COMPLETED FOR L20
L21 7 DUP REM L20 (5 DUPLICATES REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 7 ANSWERS - CONTINUE? Y/(N):y

L21 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease
locus and their use in screening for human homologs
IN ***Dove, William F.*** ; ***Shedlovsky, Alexandra***
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000004186	A1	20000127	WO 1999-US15661	19990712

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,
MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9949843	A1	20000207	AU 1999-49843	19990712
PRAI US 1998-114973	19980714			
WO 1999-US15661	19990712			

AB A method for breeding mutagenized mice that permits detection of genetic
loci that can modify a known index phenotype involves crossing a mutagenized founder strain and a second strain of mice carrying an allele
at a locus that confers the index phenotype. In the test generation, clusters of individuals are obsd. to deviate from the typical phenotype.
The genetic material and mols. encoded thereby can be obtained using
available methods. Improved and compact methods called ICMM (index-directed, cluster-enhanced, ***Modifier*** ***locus*** and
Molecule identification method) are also disclosed. The method is exemplified by identification of the suppressor or enhancer alleles of
mouse Min allele of APC locus by phenotypic and genotypic studies of F1
generation (and their outcross and backcross offsprings) of ethylnitrosourea mutagenized female BTBR and heterozygous B6-APCmin/+
male. The identification of these new genes in the mouse disease models
for human colon cancers are helpful to screen human homologs involved in
the related diseases.
RE.CNT 4
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(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Moml modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

L21 ANSWER 2 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
DUPLICATE 1
AN 2000:343967 BIOSIS
DN PREV200000343967
TI The Mom1AKR intestinal tumor resistance region consists of Pla2g2a and a
locus distal to D4Mit64.
AU Cormier, Robert T.; Bilger, Andrea; Lillich, Amy J.; Halberg, Richard B.;
Hong, Karen H.; Gould, Karen A.; Borenstein, Natalie; Lander, Eric S.;
Dove, William F. (1)
CS (1) McArdle Laboratory for Cancer Research, University of Wisconsin,
Madison, WI, 53706 USA
SO Oncogene, (29 June, 2000) Vol. 19, No. 28, pp. 3182-3192. print.
ISSN: 0950-9232.
DT Article
LA English
SL English
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during a screen for polymorphic modifiers of intestinal

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ApcMin/+ mice. Here, we demonstrate that the Mom1AKR allele consists of
two genetic components. These include the secretory phospholipase Pla2g2a,
whose candidacy as a Mom1 resistance modifier has now been tested with
several transgenic lines. A second region, distal to Pla2g2a, has also
been identified using fine structure recombinants. Pla2g2aAKR transgenic
mice demonstrate a modest resistance to tumorigenesis in the small
intestine and a very robust resistance in the large intestine. Moreover,
the tumor resistance in the colon of Pla2g2aAKR animals is
dosage-dependent, a finding that is consistent with our observation that
Pla2g2a is expressed in goblet cells. By contrast, mice carrying the
distal Mom1 modifier demonstrate a modest tumor resistance that is
confined to the small intestine. Thus, the phenotypes of these two
modifier ***loci*** are complementary, both in their
quantitative and regional effects. The additive effects and tight linkage
of these modifiers may have been necessary for the initial identification
of the Mom1 region.

L21 ANSWER 3 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:394514 BIOSIS
DN PREV199800394514
TI The intestinal epithelium and its neoplasms: Genetic, cellular and tissue
interactions.
AU ***Dove, William F.*** ; Cormier, Robert T.; Gould, Karen A.; Halberg,
Richard B.; Merritt, Anita J.; Newton, Michael A.; Shoemaker, Alexander R.
CS McArdle Lab. Cancer Res., Univ. Wisconsin, Madison, WI 53706 USA
SO Philosophical Transactions of the Royal Society of London B Biological
Sciences, (June 29, 1998) Vol. 353, No. 1370, pp. 915-923.
ISSN: 0962-8436.
DT General Review
LA English
AB The Min (multiple intestinal neoplasia) strain of the laboratory mouse and
its derivatives permit the fundamental study of factors that regulate the
transition between normal and neoplastic growth. A gene of central
importance in mediating these alternative patterns of growth is Apc, the
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adenomas form in the Min mouse, both copies of the Apc gene must be
inactivated. One copy is mutated by the nonsense Apc allele carried in
heterozygous form in this strain. The other copy can be silenced by any of
several mechanisms. These range from loss of the homologue bearing the
wild-type Apc allele; to interstitial deletions surrounding the wild-type
allele; to intragenic mutation, including nonsense alleles; and finally,
to a reduction in expression of the locus, perhaps owing to mutation in a
regulatory locus. Each of these proposed mechanisms may constitute a
two-hit genetic process as initially posited by Knudson; however,
apparently the two hits could involve either a single locus or two loci.
The kinetic order for the transition to adenoma may be still higher than
two, if polyclonal adenomas require stronger interactions than passive
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mouse is strongly dependent upon loci other than Apc. One of these, Mom1,
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the tumour (MOH or maintenance of heterozygosity). Indeed, the secretory
phospholipase is synthesized by post-mitotic Paneth cells, not by the
proliferative cells that presumably generate the tumour. An analysis of
autonomy of modifier gene action in chimeric mice deserves detailed
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chimeric and to the clonal structure of the tissue in question. Beyond
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if a candidate modifier does not explain any of the genetic epidemiology
of colon cancer in human populations, modifier activities discovered by
mouse genetics provide candidates for chemopreventive and/or therapeutic
modalities in the human.

L21 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
DUPLICATE 2
AN 1997:298155 BIOSIS
DN PREV199799597358
TI Localized gene action controlling intestinal neoplasia in mice.
AU Gould, Karen A.; ***Dove, William F. (1)***
CS (1) McArdle Lab. Cancer Res., 1400 University Ave., Madison, WI 53706 USA
SO Proceedings of the National Academy of Sciences of the United States of
America, (1997) Vol. 94, No. 11, pp. 5848-5853.
ISSN: 0027-8424.
DT Article
LA English
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L21 ANSWER 5 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
DUPLICATE 3
AN 1997:438664 BIOSIS
DN PREV199799737867
TI Secretory phospholipase Pla2g2a confers resistance to intestinal
tumorigenesis.
AU Cormier, Robert T.; Hong, Karen H.; Halberg, Richard B.; Hawkins, Trevor
L.; Richardson, Paul; Mulherkar, Rita; ***Dove, William F. (1)*** ;
Lander, Eric S.
CS (1) McArdle Lab. Cancer Research, Univ. Wisconsin, Madison, WI 53706 USA
SO Nature Genetics, (1997) Vol. 17, No. 1, pp. 88-91.
ISSN: 1061-4036.
DT Article
LA English
AB Individuals inheriting the same mutation predisposing to cancer

may show
very different outcomes, ranging from early aggressive cancer to
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tool to identify factors in the environment and genetic background that
account for such modifications. The Min mouse strain, in which the Apc-Min
mutation disrupts the mouse homologue of the human familial polyposis
gene, develops intestinal neoplasms whose multiplicity is strongly
affected by genetic background. We previously mapped a strong
modifier ***locus*** , Mom1 (modifier of Min-1), to a 4-cM
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a secretory phospholipase. Here, we report that a cosmid transgene
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comparable to that conferred by a single copy of the resistance allele of
Mom1. These results offer strong evidence that this secretory
phospholipase can provide active tumour resistance. The association of
Pla2g2a with Mom1 thus withstands a strong functional test and is likely
to represent the successful identification of a polymorphic quantitative
trait locus in mammals.

L21 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
DUPLICATE 4
AN 1996:527044 BIOSIS
DN PREV199699249400
TI Action of Min and Mom1 on neoplasia in ectopic intestinal grafts.
AU Gould, Karen A.; ***Dove, William F. (1)***
CS (1) McArdle Lab. Cancer Research, 1400 University Ave., Madison, WI 53706
USA
SO Cell Growth & Differentiation, (1996) Vol. 7, No. 10, pp. 1361-1368.
ISSN: 1044-9523.
DT Article
LA English
AB Mice heterozygous for Min, a mutant allele of Apc, develop adenomas
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cell types and seems to be involved in inflammatory responses and
bacterial defense mechanisms. Here, we determine whether Min and Mom1 act
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manner. There is no evidence that either Min or Mom1 has a systemic effect
on tumor development. However, within the colonic grafts, the Min
phenotype does not appear to be autonomous; the development of colonic
tumors in Min mice seems dependent on factors beyond the Min genotype of
the colonic epithelium. Microenvironmental factors, such as digestive
secretions, dietary components, or intestinal flora, may be critical
factors contributing to the development of Min-induced colonic tumors.
However, these factors are not required for the action of Min or Mom1
within the small intestine.

L21 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2001 BIOSIS
DUPLICATE 5
AN 1994:64047 BIOSIS
DN PREV199497077047
TI Genetic identification of Mom-1, a major ***modifier*** ***locus***
affecting Min-induced intestinal neoplasia in the mouse.
AU Dietrich, William F. (1); Lander, Eric S. (1); Smith, Jennifer S. (1);
Moser, Amy R.; Gould, Karen A.; Luongo, Cindy; Borenstein, Natalie;
Dove, William
CS (1) Whitehead Inst. Biomed Res., Dep. Biol., Mass. Inst. Technol.,
Cambridge, MA 02142 USA
SO Cell, (1993) Vol. 75, No. 4, pp. 631-639.
ISSN: 0092-8674.
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in two by a LOD score exceeding 14. Interestingly, Mom-1 intraspecific
backcrosses. The mapping is supported by a LOD score exceeding 14.
Interesting, Mom-1 lies in a region of synteny conservation with human
chromsome 1p35-36, a region of frequent somatic loss of heterozygosity in
a variety of human tumors, including colon tumors. These results provide
evidence of a major modifier affecting expression of an inherited cancer
syndrome.

=> s ethylnitrosourea/ab,bi

'AB' IS NOT A VALID FIELD CODE
L22 5586 ETHYLNITROSOUREA/AB,BI

=> s l22 and mutagen?/ab,bi

'AB' IS NOT A VALID FIELD CODE
L23 1788 L22 AND MUTAGEN?/AB,BI

=> s l23 and l9

L24 1 L23 AND L9

=> d bib ab

L24 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease
locus and their use in screening for human homologs
IN Dove, William F.; Shedlovsky, Alexandra
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000004186	A1	20000127	WO 1999-US15661	19990712

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,

MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9949843 A1 20000207 AU 1999-49843 19990712
PRAI US 1998-114973 19980714
WO 1999-US15661 19990712
AB A method for breeding ***mutagenized*** mice that permits detection of
genetic loci that can modify a known index phenotype involves crossing a
mutagenized founder strain and a second strain of mice carrying an
allele at a locus that confers the index phenotype. In the test
generation, clusters of individuals are obsd. to deviate from the typical
phenotype. The genetic material and mols. encoded thereby can be obtained
using available methods. Improved and compact methods called ICMM
(index-directed, cluster-enhanced, ***Modifier*** ***locus*** and
Molecule identification method) are also disclosed. The method is
exemplified by identification of the suppressor or enhancer alleles of
mouse Min allele of APC locus by phenotypic and genotypic studies of F1
generation (and their outcross and backcross offsprings) of
ethylnitrosourea ***mutagenized*** female BTBR and
heterozygous B6-APCmin/+ male. The identification of these new genes in
the mouse disease models for human colon cancers are helpful to screen
human homologs involved in the related diseases.
RE.CNT 4
RE
(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Moml modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

=> s l23 and backcross?/ab,bi

'AB' IS NOT A VALID FIELD CODE
L25 7 L23 AND BACKCROSS?/AB,BI

=> dup rem l25

PROCESSING COMPLETED FOR L25
L26 4 DUP REM L25 (3 DUPLICATES REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y

L26 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease
locus and their use in screening for human homologs
IN Dove, William F.; Shedlovsky, Alexandra
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI WO 2000004186 A1 20000127 WO 1999-US15661 19990712
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,
MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9949843 A1 20000207 AU 1999-49843 19990712
PRAI US 1998-114973 19980714
WO 1999-US15661 19990712
AB A method for breeding ***mutagenized*** mice that permits detection of
genetic loci that can modify a known index phenotype involves crossing a
mutagenized founder strain and a second strain of mice carrying an
allele at a locus that confers the index phenotype. In the test
generation, clusters of individuals are obsd. to deviate from the typical
phenotype. The genetic material and mols. encoded thereby can be obtained
using available methods. Improved and compact methods called ICMM
(index-directed, cluster-enhanced, Modifier locus and Molecule
identification method) are also disclosed. The method is exemplified by
identification of the suppressor or enhancer alleles of mouse Min allele
of APC locus by phenotypic and genotypic studies of F1 generation (and
their outcross and ***backcross*** offsprings) of
ethylnitrosourea ***mutagenized*** female BTBR and
heterozygous B6-APCmin/+ male. The identification of these new genes in
the mouse disease models for human colon cancers are helpful to screen
human homologs involved in the related diseases.
RE.CNT 4
RE
(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Moml modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

L26 ANSWER 2 OF 4 MEDLINE
AN 2000409356 MEDLINE
DN 20344604
TI Cryoconservation--archiving for the future.
AU Glenister P H; Thornton C E
CS MRC Mammalian Genetics Unit, Harwell, Oxon OX11 ORD, UK..
P.Glenister@har.mrc.ac.uk
SO MAMMALIAN GENOME, (2000 Jul) 11 (7) 565-71. Ref: 53
Journal code: BES. ISSN: 0938-8990.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200011
EW 20001101
AB Mouse genetics is set to play a pivotal role in the key post-genome
challenge-the study of mammalian gene function. Addressing this challenge

will involve the development and application of systematic ***mutagenesis*** approaches. The expanding mouse mutant resource that will result threatens to overwhelm the currently available animal facility space. Cryopreservation of both mouse embryos and spermatozoa is currently widely employed for the efficient archiving of mouse stocks. Distribution and dissemination of new and existing mouse strains is simplified by the availability of extensive frozen archives. Also, the availability of archives of frozen spermatozoa provides a potential powerful route for the production of ***backcross*** progeny for rapid genetic mapping. Moreover, frozen oocytes and ovaries may offer a valuable addition to the current cryopreservation approaches. Comprehensive mouse mutant archives will provide an essential resource for mammalian genetics throughout the 21(st) century.

L26 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2001 ACS
AN 1996:550637 CAPLUS
DN 125:187267
TI A high-resolution linkage map of the tight skin 2 (Tsk2) locus: a mouse model for scleroderma (SSc) and other cutaneous fibrotic diseases
AU Christner, P.J.; Siracusa, L.D.; Hawkins, D.F.; McGrath, R.; Betz, J.K.; Ball, S.T.; Jimenez, S.A.; Peters, J.
CS Jefferson Medical College, Thomas Jefferson University, Philadelphia, PA, 19107, USA
SO Mamm. Genome (1996), 7(8), 610-612
CODEN: MAMGEC; ISSN: 0938-8990
DT Journal
LA English
AB Tsk2/+ is a novel mutation that first appeared in the offspring of a male mouse from the 101/H strain that was ***mutagenized*** with ***ethylnitrosourea*** . The mouse was recognized because of the tight skin in the interscapular region. In contrast to the Tsk mutation (on chromosome 2), the Tsk2 mutation has been localized to mouse chromosome 1. The authors report the results of intraspecific and intersubspecific ***backcross*** studies performed to define the minimal region of the genome that contains the Tsk2 mutation. Thus, the position of the Tsk2 mutation was localized to the proximal region of chromosome 1. The mutation cosegregates with 4 microsatellite markers and with gene Col3a1, and is flanked on the proximal side by D1Mit233 and on the distal side by D1Mit213. These markers reside <1cM apart on the published consensus linkage map for mouse chromosome 1.

L26 ANSWER 4 OF 4 MEDLINE DUPLICATE 1
AN 88196848 MEDLINE
DN 88196848
TI hph-1: a mouse mutant with hereditary hyperphenylalaninemia induced by ***ethylnitrosourea*** ***mutagenesis*** .
AU Bode V C; McDonald J D; Guenet J L; Simon D
CS Division of Biology, Kansas State University, Manhattan 66506.
NC 5 R01 HD5354-06 (NICHD)
SO GENETICS, (1988 Feb) 118 (2) 299-305.
Journal code: FNH. ISSN: 0016-6731.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198808
AB ***Ethylnitrosourea*** ***mutagenesis*** of spermatogonial stem cells and a three-generation breeding scheme were used to screen for recessive mutations that cause defects in phenylalanine metabolism leading to elevated serum levels of this amino acid. This paper describes the isolation of such a mutation, hph-1, causing a heritable hyperphenylalaninemia in the neonate and weanling and an inability to effectively clear a phenylalanine challenge in the adult. Micro-pedigree analysis of the original mutant mouse and data obtained from crosses of affected and unaffected animals indicate that the mutation segregates in an autosomal recessive manner. An interspecies mouse ***backcross*** mapping experiment places the mutant gene locus on mouse chromosome 14 very near Np-1 and a ***backcross*** experiment with a conventional inbred mouse strain involving a nearby locus confirms the chromosome 14 assignment. The initial symptomatology of the mutant phenotype suggests this mutant may represent a useful animal model for the study of hyperphenylalaninemia in man.

=> s l9 and backcross?/ab,bi

'AB' IS NOT A VALID FIELD CODE
L27 39 L9 AND BACKCROSS?/AB,BI

=> s l27 and mutagen?/ab,bi

'AB' IS NOT A VALID FIELD CODE
L28 2 L27 AND MUTAGEN?/AB,BI

=> dup rem l28

PROCESSING COMPLETED FOR L28
L29 2 DUP REM L28 (0 DUPLICATES REMOVED)

=> d l- bib ab

YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L29 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease locus and their use in screening for human homologs
IN Dove, William F.; Shedlovsky, Alexandra
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000004186	A1	20000127	WO 1999-US15661	19990712

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9949843	A1	20000207	AU 1999-49843	19990712
PRAI US 1998-114973	19980714			
WO 1999-US15661	19990712			

AB A method for breeding ***mutagenized*** mice that permits detection of genetic loci that can modify a known index phenotype involves crossing a

mutagenized founder strain and a second strain of mice carrying an
allele at a locus that confers the index phenotype. In the test
generation, clusters of individuals are obsd. to deviate from the typical
phenotype. The genetic material and mols. encoded thereby can be obtained
using available methods. Improved and compact methods called ICMM
(index-directed, cluster-enhanced, ***Modifier*** ***locus*** and
Molecule identification method) are also disclosed. The method is
exemplified by identification of the suppressor or enhancer alleles of
mouse Min allele of APC locus by phenotypic and genotypic studies of F1
generation (and their outcross and ***backcross*** offsprings) of
ethylnitrosourea ***mutagenized*** female BTBR and heterozygous
B6-APCmin/+ male. The identification of these new genes in the mouse
disease models for human colon cancers are helpful to screen human
homologs involved in the related diseases.
RE.CNT 4
RE
(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Moml modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

L29 ANSWER 2 OF 2 MEDLINE
AN 96172827 MEDLINE
DN 96172827
TI Modulation of disease severity in cystic fibrosis transmembrane
conductance regulator deficient mice by a secondary genetic factor
[published erratum appears in Nat Genet 1996 May;13(1):129].
AU Rozmahel R; Wilschanski M; Matin A; Plyte S; Oliver M; Auerbach W; Moore
A; Forstner J; Durie P; Nadeau J; Bear C; Tsui L C
CS Department of Molecular Genetics, The University of Toronto, Ontario,
Canada.
SO NATURE GENETICS, (1996 Mar) 12 (3) 280-7.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB Mice that have been made deficient for the cystic fibrosis transmembrane
conductance regulator (Cftr) usually die of intestinal obstruction. We
have created Cftr-deficient mice and demonstrate prolonged survival among
backcross and intercross progeny with different inbred strains,
suggesting that modulation of disease severity is genetically determined.
A genome scan showed that the major ***modifier*** ***locus***
maps near the centromere of mouse chromosome 7. Electrophysiological
studies on mice with prolonged survival show that the partial
rectification of Cl- and Na+ ion transport abnormalities can be explained
in part by up-regulation of a calcium-activated Cl- conductance.
Identification of modifier genes in our Cftr(m1HSC)/Cftr(m1HSC) mice
should provide important insight into the heterogeneous disease
presentation observed among CF patients.

=> dup rem l27

PROCESSING COMPLETED FOR L27
L30 13 DUP REM L27 (26 DUPLICATES REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 13 ANSWERS - CONTINUE? Y/(N):y

L30 ANSWER 1 OF 13 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 1
AN 2001:151886 BIOSIS
DN PREV200100151886
TI Epistatic interactions between skin tumor ***modifier*** ***loci***
in interspecific (spretus/musculus) ***backcross*** mice.
AU Nagase, Hiroki; Mao, Jian-Hua; de Koning, John P.; Minami, Tomoe; Balmain,
Allan (1)
CS (1) University of California-San Francisco Comprehensive Cancer Center,
2340 Sutter Street, San Francisco, CA, 94143 USA
SO Cancer Research, (February 15, 2001) Vol. 61, No. 4, pp. 1305-1308. print.
ISSN: 0008-5472.
DT Article
LA English
SL English
AB The development of cancer is influenced both by exposure to environmental
carcinogens and by the host genetic background. Epistatic interactions
between genes are important in determining phenotype in plant and animal
systems and are likely to be major contributors to cancer susceptibility
in humans. Several tumor ***modifier*** ***loci*** have been
identified from studies of mouse models of human cancer, and genetic
interactions between ***modifier*** ***loci*** have been detected
by genome scanning using recombinant congenic strains of mice (R. Fijneman
et al., Nat. Genet., 14: 465-467, 1996; T. van Wezel et al., Nat. Genet.,
14: 468-470, 1996; W. N. Frankel et al., Nat. Genet., 14, 371-373, 1996).
We demonstrate here that strong genetic interactions between skin tumor
modifier ***loci*** can be detected by hierarchical whole
genome scanning of a complete interspecific ***backcross*** (outbred
Mus spretus X Mus musculus (NIH/Ola)). A locus on chromosome 7 (Skts1)
showed a highly significant interaction with Skts5 on chromosome 12 (P <
10-16), whereas additional significant interactions were detected between
loci on chromosomes 4 and 5, and 16 and 15. Some of these quantitative
trait loci and their interactions, in particular the Skts1-Skts5
interaction, were confirmed in two completely independent
backcrosses using inbred spretus strains (SEG/Pas and SPRET/Ei)
and NIH/Ola. These results, therefore, illustrate the general use of
interspecific crosses between Mus musculus and Mus spretus for the
detection of strong genetic interactions between tumor modifier genes.

L30 ANSWER 2 OF 13 MEDLINE DUPLICATE 2
AN 2001089278 MEDLINE
DN 20565764
TI Efficiency alleles of the Pctr1 ***modifier*** ***locus*** for
plasmacytoma susceptibility.
AU Zhang S L; DuBois W; Ramsay E S; Bliskovski V; Morse H C; Taddesse-Heath
L; Vass W C; DePinho R A; Mock B A
CS Laboratory of Genetics, Division of Basic Sciences, National Cancer
Institute, National Institutes of Health, Bethesda, Maryland 20892, USA.
SO MOLECULAR AND CELLULAR BIOLOGY, (2001 Jan) 21 (1) 310-8.

Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101
AB The susceptibility of BALB/c mice to pristane-induced plasmacytomas is a
complex genetic trait involving multiple loci, while DBA/2 and C57BL/6
strains are genetically resistant to the plasmacytomagenic effects of
pristane. In this model system for human B-cell neoplasia, one of the
BALB/c susceptibility and ***modifier*** ***loci*** , Pctr1, was
mapped to a 5.7-centimorgan (cM) chromosomal region that included Cdkn2a,
which encodes p16(INK4a) and p19(ARF), and the coding sequences for the
BALB/c p16(INK4a) and p19(ARF) alleles were found to be polymorphic with
respect to their resistant Pctr1 counterparts in DBA/2 and C57BL/6 mice
(45). In the present study, alleles of Pctr1, Cdkn2a, and D4Mit15 from a
resistant strain (BALB/cDAG) carrying DBA/2 chromatin were introgressively
backcrossed to the susceptible BALB/c strain. The resultant
C.DAG-Pctr1 Cdkn2a D4Mit15 congenic was more resistant to
plasmacytomagenesis than BALB/c, thus narrowing Pctr1 to a 1.5-cM
interval. Concomitantly, resistant C57BL/6 mice, from which both gene
products of the Cdkn2a gene have been eliminated, developed
pristane-induced plasma cell tumors over a shorter latency period than the
traditionally susceptible BALB/cAn strain. Biological assays of the
p16(INK4a) and p19(ARF) alleles from BALB/c and DBA/2 indicated that the
BALB/c p16(INK4a) allele was less active than its DBA/2 counterpart in
inducing growth arrest of mouse plasmacytoma cell lines and preventing
ras-induced transformation of NIH 3T3 cells, while the two p19(ARF)
alleles displayed similar potencies in both assays. We propose that the
BALB/c susceptibility/ ***modifier*** ***locus*** , Pctr1, is an
"efficiency" allele of the p16(INK4a) gene.

L30 ANSWER 3 OF 13 CAPLUS COPYRIGHT 2001 ACS
AN 2000:68594 CAPLUS
DN 132:103741
TI Method for identifying mutant alleles of mouse affecting a genetic disease
locus and their use in screening for human homologs
IN Dove, William F.; Shedlovsky, Alexandra
PA Wisconsin Alumni Research Foundation, USA
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000004186	A1	20000127	WO 1999-US15661	19990712

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS,
JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,
MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9949843	A1	20000207	AU 1999-49843	19990712
PRAI US 1998-114973	19980714			
WO 1999-US15661	19990712			

AB A method for breeding mutagenized mice that permits detection of genetic
loci that can modify a known index phenotype involves crossing a
mutagenized founder strain and a second strain of mice carrying an allele
at a locus that confers the index phenotype. In the test generation,
clusters of individuals are obsd. to deviate from the typical phenotype.
The genetic material and mols. encoded thereby can be obtained using
available methods. Improved and compact methods called ICMM
(index-directed, cluster-enhanced, ***Modifier*** ***locus*** and
Molecule identification method) are also disclosed. The method is
exemplified by identification of the suppressor or enhancer alleles of
mouse Min allele of APC locus by phenotypic and genotypic studies of F1
generation (and their outcross and ***backcross*** offsprings) of
ethylnitrosourea mutagenized female BTBR and heterozygous B6-APCmin/+
male. The identification of these new genes in the mouse disease models
for human colon cancers are helpful to screen human homologs involved in
the related diseases.
RE.CNT 4
RE
(1) Anon; GENETICS 1996, V144(4), P1777
(2) Dietrich, W; "GENETIC IDENTIFICATION OF MOM-1, A MAJOR MODIFIER LOCUS
AFFECTING MIN-INDUCED INTESTINAL NEOPLASIA IN THE MOUSE" CELL V75, P631
CAPLUS
(3) Gould, K; Genetic evaluation of candidate genes for the Moml modifier of
intestinal neoplasia in mice
(4) Wisconsin Alumni Res Found; WO 9822622 A 1998 CAPLUS

L30 ANSWER 4 OF 13 MEDLINE DUPLICATE 3
AN 2001101547 MEDLINE
DN 20545364
TI Mapping of melanoma ***modifier*** ***loci*** in RET transgenic
mice.
AU Dragani T A; Peissel B; Zanesi N; Aloisi A; Dai Y; Kato M; Suzuki H;
Nakashima I
CS Department of Experimental Oncology, Istituto Nazionale Tumori, Via G.
Venezian Milan, Italy.. dragani@istitutotumori.mi.it
SO JAPANESE JOURNAL OF CANCER RESEARCH, (2000 Nov) 91 (11) 1142-7.
Journal code: HBA. ISSN: 0910-5050.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200102
AB Transgenic mice carrying the RET oncogene under the control of the
metallothionein promoter exhibit severe pigmentation of the whole skin and
melanocytic tumors. The genetic background influences melanoma development
in RET mice; founder mice crossed with BALB/c mice show decreased
incidence and increased latency of melanocytic tumors, whereas progeny of
C57BL/6 mice show the opposite effect. Using partially congenic RET mice
on a C57BL/6 genetic background (N3/RET mice), we studied genetic linkage
in (N3/RETxBALB/c)xN3/RET ***backcross*** mice. We mapped three
melanoma ***modifier*** ***loci*** , on chromosome 1 (Melm1 and
Melm2) and chromosome 11 (Melm3), that are linked with early melanoma
incidence and latency. Mapping of Melm loci and of five additional

regions
on chromosomes 6, 8, 9, 12, and 13 indicated allelic imbalance in N3/RET
mice, with a significant excess of BALB/c alleles, suggesting the presence
of additional putative melanoma ***modifier*** ***loci*** on these
chromosomes.

L30 ANSWER 5 OF 13 CAPLUS COPYRIGHT 2001 ACS
AN 2000:80654 CAPLUS
DN 132:235822
TI Genetic regulation of anti-erythrocyte autoantibodies and splenomegaly in
autoimmune hemolytic anemia-prone New Zealand Black mice
AU Ochiai, Kimiko; Ozaki, Shoichi; Tanino, Akihiro; Watanabe, Shinji; Ueno,
Tomoo; Mitsui, Kenichi; Toei, Junichi; Inada, Yuji; Hirose, Sachiko;
Shirai, Toshikazu; Nishimura, Hiroyuki
CS Toin Human Science and Technology Center, Department of Biomedical
Engineering, Toin University of Yokohama, Yokohama, 225-8502, Japan
SO Int. Immunol. (2000), 12(1), 1-8
CODEN: INIMEN; ISSN: 0953-8178
PB Oxford University Press
DT Journal
LA English
AB New Zealand Black (NZB) mice spontaneously produce anti-erythrocyte
autoantibodies (AEA) in assocn. with splenomegaly, thus serving as a model
for autoimmune hemolytic anemia. Although these autoimmune traits are
inherited as a dominant fashion, expression in F1 hybrids of NZB and most
non-New Zealand strains is suppressed due to the contribution of wild-type
modifying genes present in the latter strains. Using chromosomal
microsatellite markers in the (C57BL/6 .times. NZB)F1 .times. NZB
backcross progeny, the authors mapped C57BL/6 modifying loci for
AEA prodn. and splenomegaly. Generation of AEA was down-regulated by a
combined effect of two major independently segregating dominant alleles,
one linked to D7MIT30 on chromosome 7 and the other linked to D10MIT42 on
chromosome 10. Splenomegaly was modified mainly by a single C57BL/6
allele linked to D4MIT58 on chromosome 4. Thus, the autoimmune hemolytic
anemia in the NZB strain is under multigenic control and a combined action
of not only susceptibility but also modifying alleles with suppressive
activities affects the outcome of disease features in the progeny. There
are potentially important candidate genes which may be linked to the
regulation of AEA and splenomegaly.
RE.CNT 31
RE
(4) Dietrich, W; Genetics 1992, V131, P423 CAPLUS
(5) Drake, C; Proc Natl Acad Sci USA 1994, V91, P4062 CAPLUS
(7) Egle, A; Eur J Immunol 1996, V26, P3119 CAPLUS
(9) Hirose, S; Int Immunol 1994, V6, P1857 CAPLUS
(12) Jiang, Y; J Immunol 1997, V158, P992 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 6 OF 13 MEDLINE DUPLICATE 4
AN 2000079602 MEDLINE
DN 20079602
TI A subset of skin tumor ***modifier*** ***loci*** determines
survival time of tumor-bearing mice.
AU Nagase H; Mao J H; Balmain A
CS University of California San Francisco Cancer Center, Cancer Research
Institute, University of California, 2340 Sutter Street, San Francisco, CA
94105, USA.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1999 Dec 21) 96 (26) 15032-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 200003
EW 20000305
AB Studies of mouse models of human cancer have established the existence of
multiple tumor modifiers that influence parameters of cancer
susceptibility such as tumor multiplicity, tumor size, or the probability
of malignant progression. We have carried out an analysis of skin tumor
susceptibility in interspecific Mus musculus/Mus spretus hybrid mice and
have identified another seven loci showing either significant (six loci)
or suggestive (one locus) linkage to tumor susceptibility or resistance. A
specific search was carried out for skin tumor ***modifier*** ***loci*** associated with time of survival after development of a
malignant tumor. A combination of resistance alleles at three markers
[D6Mit15 (Skts12), D7Mit12 (Skts2), and D17Mit7 (Skts10)], all of which
are close to or the same as loci associated with carcinoma incidence
and/or papilloma multiplicity, is significantly associated with increased
survival of mice with carcinomas, whereas the reverse combination of
susceptibility alleles is significantly linked to early mortality caused
by rapid carcinoma growth (chi(2) = 25.22; P = 5.1 x 10(-8)). These data
indicate that host genetic factors may be used to predict carcinoma growth
rate and/or survival of individual ***backcross*** mice exposed to the
same carcinogenic stimulus and suggest that mouse models may provide an
approach to the identification of genetic modifiers of cancer survival in
humans.

L30 ANSWER 7 OF 13 MEDLINE DUPLICATE 5
AN 1998054360 MEDLINE
DN 98054360
TI Epilepsy in mice deficient in the 65-kDa isoform of glutamic acid decarboxylase.
AU Kash S F; Johnson R S; Tecott L H; Noebels J L; Mayfield R D; Hanahan D;
Baekkeskov S
CS Department of Medicine, School of Medicine, University of California at
San Francisco, San Francisco, CA 94143, USA.
NC DK41822 (NIDDK)
NS29709/11535 (NINDS)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1997 Dec 9) 94 (25) 14060-5.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199803
EW 19980303
AB gamma-Aminobutyric acid (GABA), the major inhibitory neurotransmitter in
the mammalian brain, is synthesized by two glutamate decarboxylase
isoforms, GAD65 and GAD67. The separate role of the two isoforms is
unknown, but differences in saturation with cofactor and subcellular
localization suggest that GAD65 may provide reserve pools of GABA for
regulation of inhibitory neurotransmission. We have disrupted the gene
encoding GAD65 and ***backcrossed*** the mutation into the C57BL/6
strain of mice. In contrast to GAD67-/- animals, which are born

with
developmental abnormalities and die shortly after birth, GAD65-/- mice
appear normal at birth. Basal GABA levels and holo-GAD activity are
normal, but the pyridoxal 5' phosphate-inducible apo-enzyme reservoir is
significantly decreased. GAD65-/- mice develop spontaneous seizures that
result in increased mortality. Seizures can be precipitated by fear or
mild stress. Seizure susceptibility is dramatically increased in GAD65-/-
mice ***backcrossed*** into a second genetic background, the nonobese
diabetic (NOD/LtJ) strain of mice enabling electroencephalogram analysis
of the seizures. The generally higher basal brain GABA levels in this
backcross are significantly decreased by the GAD65-/- mutation,
suggesting that the relative contribution of GABA synthesized by GAD65 to
total brain GABA levels is genetically determined. Seizure-associated
c-fos-like immunoreactivity reveals the involvement of limbic regions of
the brain. These data suggest that GABA synthesized by GAD65 is important
in the dynamic regulation of neural network excitability, implicate at
least one ***modifier*** ***locus*** in the NOD/LtJ strain, and
present GAD65-/- animals as a model of epilepsy involving GABA-ergic
pathways.

L30 ANSWER 8 OF 13 MEDLINE DUPLICATE 6
AN 96172827 MEDLINE
DN 96172827
TI Modulation of disease severity in cystic fibrosis transmembrane conductance regulator deficient mice by a secondary genetic factor [published erratum appears in Nat Genet 1996 May;13(1):129].
AU Rozmahel R; Wilschanski M; Matin A; Plyte S; Oliver M; Auerbach W; Moore
A; Forstner J; Durie P; Nadeau J; Bear C; Tsui L C
CS Department of Molecular Genetics, The University of Toronto, Ontario,
Canada.
SO NATURE GENETICS, (1996 Mar) 12 (3) 280-7.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB Mice that have been made deficient for the cystic fibrosis transmembrane
conductance regulator (Cftr) usually die of intestinal obstruction. We
have created Cftr-deficient mice and demonstrate prolonged survival among
backcross and intercross progeny with different inbred strains,
suggesting that modulation of disease severity is genetically determined.
A genome scan showed that the major ***modifier*** ***locus***
maps near the centromere of mouse chromosome 7. Electrophysiological
studies on mice with prolonged survival show that the partial
rectification of Cl- and Na+ ion transport abnormalities can be explained
in part by up-regulation of a calcium-activated Cl- conductance.
Identification of modifier genes in our Cftr(m1HSC)/Cftr(m1HSC) mice
should provide important insight into the heterogeneous disease
presentation observed among CF patients.

L30 ANSWER 9 OF 13 MEDLINE DUPLICATE 7
AN 96121384 MEDLINE
DN 96121384
TI A curly-tail ***modifier*** ***locus*** , mct1, on mouse chromosome
17.
AU Letts V A; Schork N J; Copp A J; Bernfield M; Frankel W N
CS Jackson Laboratory, Bar Harbor, Maine 04609, USA.
NC HD28882 (NICHD)
SO GENOMICS, (1995 Oct 10) 29 (3) 719-24.
Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB The major gene for neural tube defects, ct, in the curly-tail (CT) mouse
strain was mapped previously to mouse chromosome 4 by combining linkage
data from several ***backcrosses*** . The penetrance of the neural tube
trait, already incomplete in the CT strain, was further reduced in several
of these ***backcrosses*** , suggesting the existence of recessive
modifiers or strain-specific susceptibility alleles. Here we describe the
mapping of a curly-tail ***modifier*** ***locus*** , mct1, to
chromosome 17 in moderate and low penetrance crosses of CT with BALB/cByJ
and Mus spretus. No effect of mct1 was seen in a higher penetrance cross
with the BXD-8/Ty strain, confirming that ct is the major gene in the
model. Homozygosity at both ct and mct1 loci was sufficient to account for
all of the affected individuals in the BALB/cByJ cross and most of the
affected individuals in the M. spretus cross and was the preferred model
overall. No evidence was found for epistatic interaction between ct and
mct1.

L30 ANSWER 10 OF 13 MEDLINE DUPLICATE 8
AN 96106991 MEDLINE
DN 96106991
TI Steroid sulfatase and the Y chromosome hypertensive locus of the spontaneously hypertensive rat.
AU Johnson M L; Ely D L; Turner M E
CS Midwest Hypertension Research Center, Omaha, Nebraska, USA.
SO STEROIDS, (1995 Oct) 60 (10) 681-5.
Journal code: V10. ISSN: 0039-128X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199604
AB The spontaneously hypertensive rat (SHR) has a Y chromosome locus that
increases blood pressure. This locus requires an androgen receptor and
testosterone for maximum expression. Steroid sulfatase (STS) catalyzes the
conversion of steroid sulfates to their active nonconjugated form. In some
mammals the steroid sulfatase locus (Sts) is on the Y chromosome, although
the rat Sts is on the X chromosome. We measured STS activity levels in SHR
and normotensive Wistar Kyoto (WKY) males. SHR had significantly higher
STS activity in testes, adrenal gland, liver, and hypothalamus. The Km
values for STS in the two strains were not significantly different; thus,
activity differences were likely due to differences in enzyme amounts. STS
activity was measured in the ***backcross*** strains SHR/y and SHR/a
to test and/or confirm a Y chromosome influence on STS. STS activity
levels in these strains were intermediate between those of SHR and WKY.
Because the blood pressures of SHR/y and SHR/a were also intermediate
between SHR and WKY, the STS activity could be a secondary response to the

hypertension. An alternative hypotheses is that a regulatory locus in addition to the structural locus is responsible for STS activity levels, and this regulatory locus is on the rat Y chromosome. Further study is needed to discriminate between these possibilities, and until the second hypothesis can be eliminated, the Sts locus or its ***modifier*** ***loci*** remain a potential component of the Y chromosome hypertensive locus.

L30 ANSWER 11 OF 13 MEDLINE DUPLICATE 9
AN 94061981 MEDLINE
DN 94061981
TI Genetic identification of Mom-1, a major ***modifier*** ***locus*** affecting Min-induced intestinal neoplasia in the mouse.
AU Dietrich W F; Lander E S; Smith J S; Moser A R; Gould K A; Luongo C; Borenstein N; Dove W
CS Whitehead Institute for Biomedical Research, Massachusetts Institute of Technology, Cambridge 02142.
NC HG00098 (NHGRI)
HG00126 (NHGRI)
CA07075 (NCI)
+
SO CELL, (1993 Nov 19) 75 (4) 631-9.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199403
AB Mutations in the human APC gene caused various familial colon cancer syndromes. The Multiple intestinal neoplasia (Min) mouse provides an excellent model for familial colon cancer: it carries a mutant mouse Apc gene and develops many intestinal adenomas. Here, we analyze how this tumor phenotype is dramatically modified by genetic background. We report the genetic mapping of a locus that strongly modifies tumor number in Min/+ animals. This gene, Mom-1 (Modifier of Min-1), maps to distal chromosome 4 and controls about 50% of genetic variation in tumor number in two intraspecific ***backcrosses*** . The mapping is supported by a LOD score exceeding 14. Interestingly, Mom-1 lies in a region of synteny conservation with human chromosome 1p35-36, a region of frequent somatic loss of heterozygosity in a variety of human tumors, including colon tumors. These results provide evidence of a major modifier affecting expression of an inherited cancer syndrome.

L30 ANSWER 12 OF 13 MEDLINE DUPLICATE 10
AN 92176249 MEDLINE
DN 92176249
TI The Min (multiple intestinal neoplasia) mutation: its effect on gut epithelial cell differentiation and interaction with a modifier system.
AU Moser A R; Dove W F; Roth K A; Gordon J I
CS McArdle Laboratory, University of Wisconsin, Madison 53706..
NC CA07075 (NCI)
CA50585 (NCI)
CA23076 (NCI)
+
SO JOURNAL OF CELL BIOLOGY, (1992 Mar) 116 (6) 1517-26.
Journal code: HMV. ISSN: 0021-9525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199206
AB Min is a fully penetrant dominant mutation that leads to the development of multiple intestinal adenomas throughout the duodenal-to-colonic axis. Min/+ C57BL6/J mice have an average life-span of 120 d. Multi-label immunocytochemical studies of these lesions demonstrate patches of differentiated enterocytes, and scattered enteroendocrine, goblet and Paneth cells. Expression of endogenous marker genes within these differentiated cells can be directly correlated with the position occupied by the adenoma along the duodenal-to-colonic axis and mirrors the regional differentiation of the normal gut epithelium. The presence of multiple lineages in adenomas together with their retention of spatial information suggests that tumorigenesis in Min/+ mice may be initiated in a multipotent stem cell normally located at the base of intestinal crypts. To study the time-dependent properties of these tumors, genetic conditions were sought in which Min/+ animals could survive for up to 300 d. Min is fully penetrant in hybrids with either AKR/J or MA/MyJ. However, the hybrids demonstrate a reduction in the number of intestinal adenomas. Preliminary ***backcross*** analysis is consistent with a single major ***modifier*** ***locus*** unlinked to Min in both the AKR/J and MA/MyJ strains. The increased lifespan of the hybrid animals is also associated with the development of invasive tumors. New tumors do not arise continuously over the lifespan of these animals; instead all adenomas appear to be established by 100 d of age or sooner. These studies indicate that the Min/+ mouse is a powerful model system for analyzing the mechanisms that establish and maintain a balance between proliferation and differentiation in the continuously renewing gut epithelium and for an assessment of the multi-step hypothesis of intestinal neoplasia.

L30 ANSWER 13 OF 13 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1990:43589 BIOSIS
DN BA89:20953
TI EVALUATION OF F-2 X F-2 AND BC-1 X BC-1 MAIZE INTERPOPULATION CROSSES.
AU BERNARDO R; JOHNSON G R; DUDLEY J W; MEGHJI M R
CS DEP. AGRON., UNIV. ILL., 1102 S. GOODWIN AVE., URBANA, ILL. 61801.
SO CROP SCI, (1989) 29 (6), 1377-1381.
CODEN: CRPSAY. ISSN: 0011-183X.
FS BA; OLD
LA English
AB Further improvement in the performance of elite maize (Zea mays L.) hybrids is an important objective of maize breeding programs. Introgression of broadbase germplasm to improve the elite single cross B73 .times. Mo17H was considered. Estimates of genetic parameters in a [B73 73 .times. B Composite]F2 .times. [Mo17H .times. A Composite]F2 Design 2 population and a [B73(B73 .times. B Composite]BC1 .times. [Mo17H(Mo17H .times. A Composite)]BC1 Design 2 population were obtained. Proportion of broadbase germplasm had a linear effect on means with the order of performance (most favorable to least favorable) for all traits being B73 .times. Mo17H, the BC1 interpopulation cross, the F2 interpopulation cross, and A Composite .times. B Composite. Estimates of half-sib covariances (CovHS) and specific combining ability variance (VarSCA) for grain moisture and plant and ear heights were greater in the F2 than in the BC1 interpopulation cross as expected for a one-locus, two-allele genetic model. Contrary to expectations, estimates for grain yield of

CovHS in the population related to B73 and of VarSCA were two and four
times greater, respectively, in the BC1 than in the F2. The large
estimates of CovHS and VarSCA for grain yield in the BC, interpopulation
cross were consistent with expectations for a model in which B73 and Mo17H
are homozygous for an allele at a ***modifier*** ***locus***
.
which causes complete dominance at a quantitative trait locus. Frequency
of the modifier allele in the two composites would be near zero under this
model. The VarSCA results suggested the use of ***backcross***
populations for selection procedures that exploit specific combining
ability efects. Together with higher frequencies of BC1 .times. BC1
testcrosses superior to B73 .times. Mo17H, they indicated a higher
probability for immediate derivation of superior single crosses from the
BC1.

=> d his

(FILE 'HOME' ENTERED AT 16:41:46 ON 02 APR 2001)

FILE 'MEDLINE' ENTERED AT 16:41:53 ON 02 APR 2001
L1 0 S CONGENIC AND MUTAGENESIS MAPPING/AB,BI
L2 3 S MUTAGENESIS MAPPING/AB,BI
L3 108 S MODIFIER LOCUS OR MODIFIER LOCI/AB,BI
L4 10 S L3 AND CONGEN?/AB,BI
L5 4 S L4 AND MAP?/AB,BI
L6 0 S L3 AND L2

FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS' ENTERED AT 16:46:21 ON 02
APR 2001
L7 0 S L1
L8 42 S L2
L9 442 S L3
L10 62 S L4
L11 484 S L8 OR L9 OR L10
L12 39 S L11 AND BACKCROSS?/AB,BI
L13 13 DUP REM L12 (26 DUPLICATES REMOVED)
E DOVE WILLIAM F/AU
L14 133 S E2-E3
L15 12 S L14 AND L3
L16 7 DUP REM L15 (5 DUPLICATES REMOVED)
L17 0 S L14 AND L2
L18 0 S L14 AND L10
E SHEDLOVSKY ALEXANDRA/AU
L19 88 S E1-E4
L20 12 S L11 AND (L19 OR L14)
L21 7 DUP REM L20 (5 DUPLICATES REMOVED)
L22 5586 S ETHYLNITROSOUREA/AB,BI
L23 1788 S L22 AND MUTAGEN?/AB,BI
L24 1 S L23 AND L9
L25 7 S L23 AND BACKCROSS?/AB,BI
L26 4 DUP REM L25 (3 DUPLICATES REMOVED)
L27 39 S L9 AND BACKCROSS?/AB,BI
L28 2 S L27 AND MUTAGEN?/AB,BI
L29 2 DUP REM L28 (0 DUPLICATES REMOVED)
L30 13 DUP REM L27 (26 DUPLICATES REMOVED)

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

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FULL ESTIMATED COST	149.64	153.29

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